

FIG. 1A

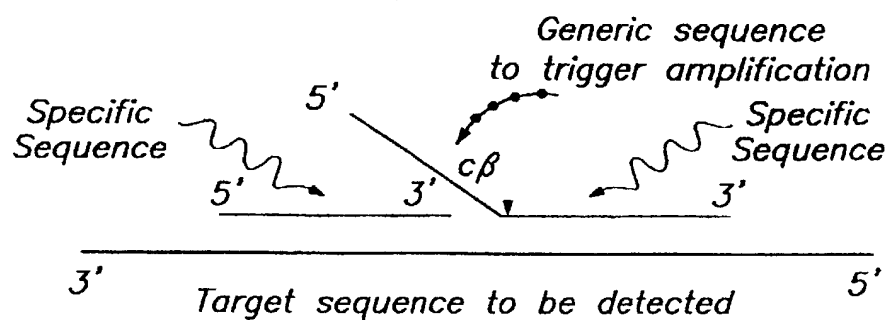


FIG. 1B PART ONE: TRIGGER REACTION

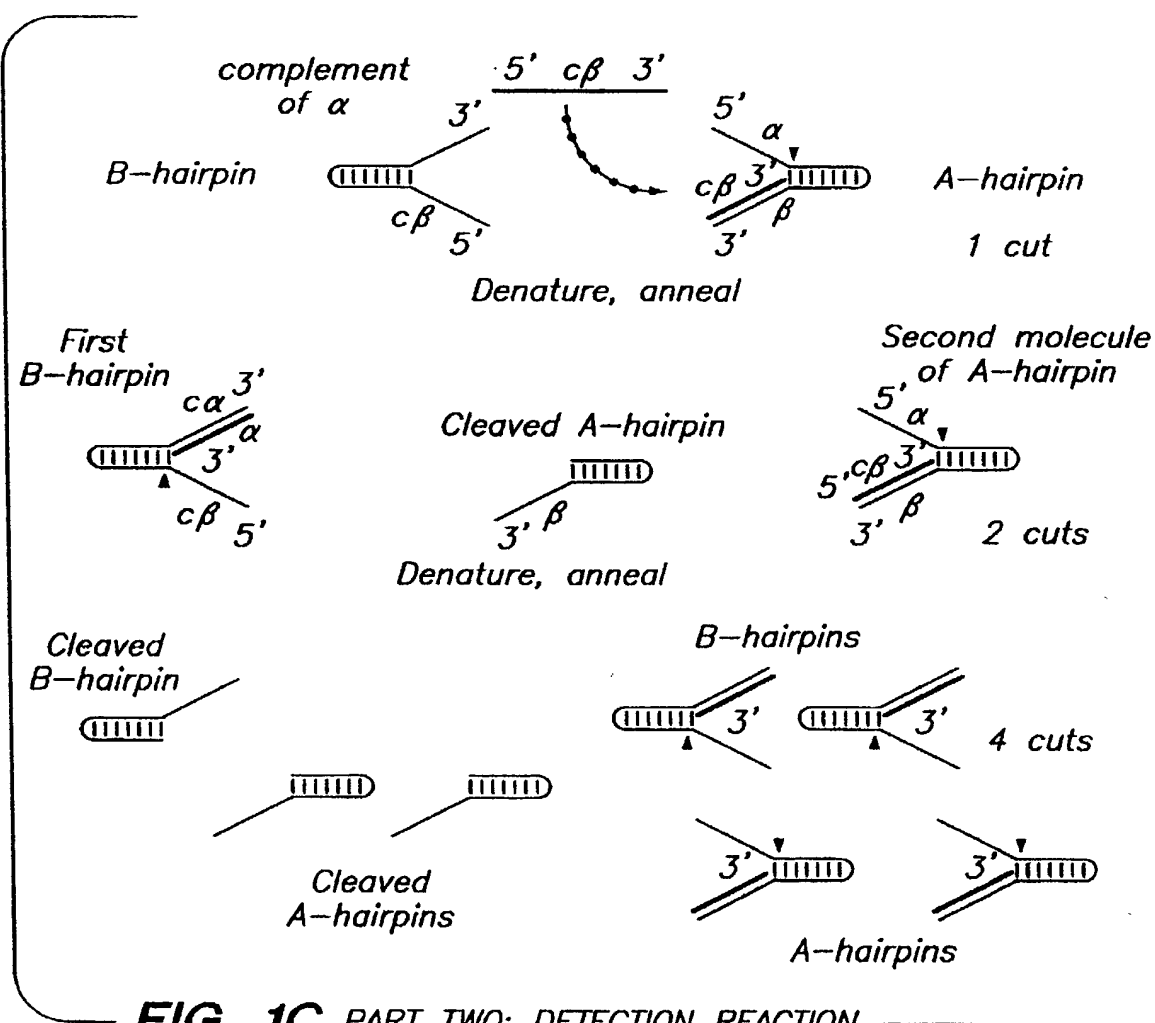


FIG. 1C PART TWO: DETECTION REACTION

FIG. 2A

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MAJORITY [SEQ ID NO:7] ATGXXGGCGATGCTTCCCGCTGTTGAGCCCAAGGCGCGGTGCTCCTGGTGGAGCGGCGCACCACTGGCGT
DNAPTAO [SEQ ID NO:1] ... AG..G.....G.....G..... 70
DNAPTFL [SEQ ID NO:2] ... ..C.....C..G..... 67
DNAPTTH [SEQ ID NO:3] ... GA.....G.....A..... 70

MAJORITY ACCGCACCTTCTTGGCCCTGAAGGGCTCAGCAGCAGCGGGGGGGAACCGGTGCAGGGGCTCTACGGCTT
DNAPTAO .....CA.....G..G..... 140
DNAPTFL .....T.....C.....C.....C..T..... 137
DNAPTTH .....G..... 140

MAJORITY CGCCAAGAGGCTCCTCAAGGCCCTGAAGGAGGACGGGGACXXGGCGGTGCTGCTTTGAGGCGCAAG
DNAPTAO .....C.....A..... 207
DNAPTFL .....A.....GT..T..... 204
DNAPTTH .....T..AA..C..CT..... 210

MAJORITY GCGCCCTCCTTCGGCCACGAGGCCCTAGGAGGCCCTACAAGCGCGGGCGGGCCCGCCCGGAGGACCTTC
DNAPTAO .....G..GG.....G..... 277
DNAPTFL .....DNAPTFL..... 274
DNAPTTH .....GA.....G.....C.. 280

MAJORITY CCGGGCAGCTCGCCCTCATCAAGGAGCTGCTGGACCTCCTGGGGCTTGGCGGGCTCGAGGTCCCGGGGCTA
DNAPTAO .....A.....G.....G..... 347
DNAPTFL .....G.....T.....A..G..T..G..G..T..... 344
DNAPTTH .....T.....T..A.C..... 350

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CGCGGGCTCGAGGTCCCGCCCGGCGGGCGGGGACXXGGCGGTGCTGCTTTGAGGCGCAAG

$$\frac{d^2 \psi}{dt^2} = -\omega^2 \psi$$

ONAPTAQ [SEQ ID NO:1]	G.	G.	C.	417
ONAPTFL [SEQ ID NO:2]	T.	G.	C.	414
ONAPTTH [SEQ ID NO:3]	.	T.	C.	420

DNAPTAC	AAA.	T.	CA.	487
DNAPTFL	T.		G. G.	484
DNAPTTH		A.	G. G.	490

DNAPIAQ	C.	A.	C.	C.	CG.	A.	557
DNAPTFL		AC.		C.	C.		554
DNAPTTH	A.			C.		T.	560

DNAPIAQ	G. GAG. T.	G. GAG. T.	627
DNAPIEL G. T. A.	A. G. A.	624
DNAPIH T.	T.	630

DNAPTAG	GC.....C.....A.....	694
DNAPTFL	T.C.C.....T.....T.G.	C 691
DNAPTTR	A.....A.....A.....C	700

[illegible]

—

FIG. 2D

MAJORITY [SEQ ID NO:7]	CGGGGXTCTCCTCGCGAAGGAGCTGGCGTTTGGCGCTGAAGGAGGGCCTXGACCTCXTGCGCGGGGACG	
DNAPTAQ [SEQ ID NO:1]G..T.....A.....AG.....C.....A.....T..G.....CC.....C.....	1114
DNAPTFL [SEQ ID NO:2]AA.....G.....G.....G.....C.....G.....T..C...A..A.....	1111
DNAPTTH [SEQ ID NO:3]C.....C.....C.....C.....TC.....G..A.....G.....	1120
MAJORITY	ACCCCATGCTGCTCGGCTAGCTCCTGGAGCCCTCGAACACGACCCCGAGGGGCTGCGCCGCGGCTACGG	
DNAPTAQG.....T.....T.....	1184
DNAPTFLG.....T.....T.....T.....T.....	1181
DNAPTTHG.....G.....G.....	1190
MAJORITY	GGGGGAGTGGACCGAGGAXGGGGGGAGCGGGCGCTGCTXTGGAGAGGGCTCTTCCXGAACCTXXGGGAG	
DNAPTAQ	C.....G.....G.....GC.....T.....GGC.....GTG...G..	1254
DNAPTFLT.....A.....GG.....C..C.....A..C...AAA....	1251
DNAPTTHC..C.CCC.C.....C..G.....CAT..G.....CCTTA..	1260
MAJORITY	CGGCTTGAAGGGAGGAGGGCTCCTTTGGCTTACGAGGAGGTGGAGAGCCGCTTTCGCGGGTGGTGG	
DNAPTAQ	A..G.....A.....A.....G.....G.....GCT.....	1324
DNAPTFLA.....A..A..AG.C..G.....G.....G.....GT...	1321
DNAPTTHC.....A.....C.....C.....A.....C.....	1330
MAJORITY	CCACATGGAGCGGCACCGGGGTGCGGGCTGGAGGTGGGCTACCTCGAGGCGCTTCCCTGGAGGTGGCGGA	
DNAPTAQG..C.....G..C.....T...AG.....T..G.....C...	1394
DNAPTFLGG.....C.....C.....C.....C.....A...G	1391
DNAPTTHC.....A.....A.....T.....T.....C.T.....	1400

CGGCTTGAAGGGAGGAGGGCTCCTTTGGCTTACGAGGAGGTGGAGAGCCGCTTTCGCGGGTGGTGG

[illegible]

DNAPTAQ	[SEQ ID NO:1]	GC.....CC.....	1464
DNAPTFL	[SEQ ID NO:2]	GC.....AG..G.....	1461
DNAPTTH	[SEQ ID NO:3]T.....G.....	1470

DNAPTAQ	C.	A.	G.	1534
DNAPTFL	GC.	G. C. G. T.	G. G. A.	1531
DNAPTTH		TA.	T. G. G. C. A.	1540

DNAPTAQ	G.	G.	G.	1604
DNAPTFL	T.	G.	CCG.	1601
DNAPTTH	G.	A.	G.	1610

DNAPTAC	G.	G.	T.	G.A.	A.	1674
DNAPTFL			A.	C.C.	G.	1671
DNAPTTH			G.G.	C.AAG.	G.	1680

DNAPTAQ	A	I	G.	1744
DNAPTFL	G.	C	TC		1741
DNAPTTH		G			1750

FIG. 2G

MAJORITY [SEQ ID NO:7]	AGCTTCCCAAGGTCCGCGCCTGGATTGAGAGACCCCTGGAGGAGCGGCAAGAGCGGGGTACGTGGAGA	2164
DNAPTAQ [SEQ ID NO:13]	2164
DNAPTFL [SEQ ID NO:2]A.....GG.....C.....C.CC.....T.....	2161
DNAPTTR [SEQ ID NO:3]A.....A.....G.....A.....C.....A.....	2170
MAJORITY	CGCTCTTGGCGCGCGCGGCTACGTGCCCGAGCTCAAGCGCCGGGTGAAGAGCCGTCCGCGGAGCGCGCGCGGA	
DNAPTAQC.....A.....AG.G.....C.....	2234
DNAPTFLT.....C.....	2231
DNAPTTRAA.AA.....CA.....C.....	2240
MAJORITY	CGGCATGGCCCTTCAACATGCCCGTCCAGCGGCACCGCGCGGACCTCATGAAGCTGGCCCATGGTGAAGCTC	
DNAPTAQT.....	2304
DNAPTFLG.....CG...T	2301
DNAPTTRC.....	2310
MAJORITY	TTCGCCCGGCTXCAGGAAATCGGCGCCAGGATGCTGCTXCAGGTCACGAGGAGCTGGTCTCGAGGCGCG	
DNAPTAQA.....GG.....T.....	2374
DNAPTFLT.....C.....G.....TT.G.....G.....	2371
DNAPTTRC..C.G..G.....C.C.....C.....CC.....G.....	2380
MAJORITY	CCAAAGAGCGCGCGGAGGCGGTGGCCGCTTTGCCCAAGGAGGTGATGGAGGGGGTCTATCCCCCTGGCCGT	
DNAPTAQA.....A.....CC.....CGGC.....G.....	2444
DNAPTFLG..C.....AG..A.....GG.....CAG..	2441
DNAPTTRC...C.....C...A.....G.....C.....AA..C.....C.....	2450

[illegible]

100

[illegible]

1

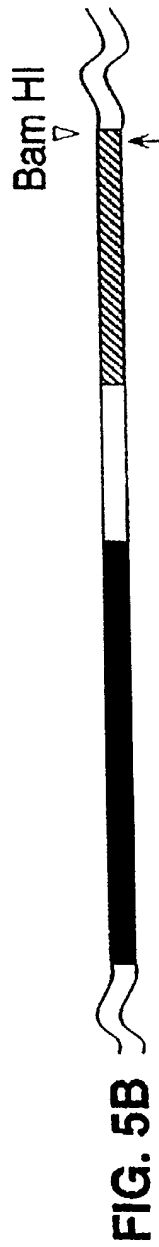
[illegible]

FIG. 3C

MAJORITY	[SEQ ID NO:8]	SFPKVRAWIEKTEEGRRRGYVETLFGRRRYVPDLNARVKSUREAAERMAFNMPVGGTAADLKKLAMVKL	
TAQ PRO	[SEQ ID NO:4]E.....	768
TFL PRO	[SEQ ID NO:5]G.....Y.....R.....	767
TTM PRO	[SEQ ID NO:6]K.....	770
MAJORITY FPRLEXMGARM LQVHDELVL EAPKXRAEXVAALAKEVMEGVYPLAVPLEVEVGXGEDWLSAKEX			
TAQ PROE.....E...A...R.....I.....		833
TFL PROO.L.....D...R.....W.O.....L.....		831
TTM PROR.....L.....OA...E...A...KA.....M.....G		835

400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500

(The following information was obtained from the records of the FBI, Department of Justice, dated 7-10-68.)



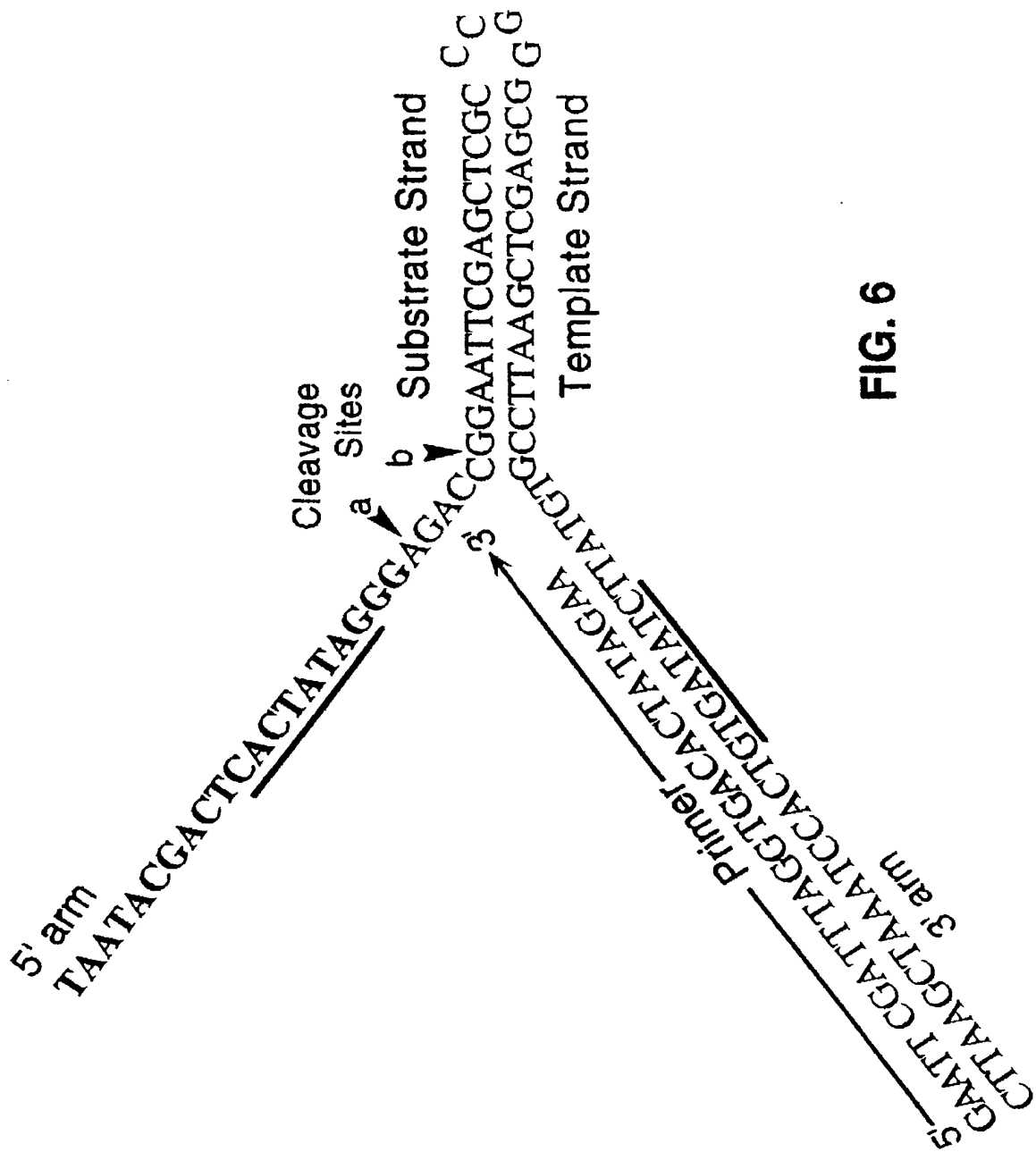


FIG. 6

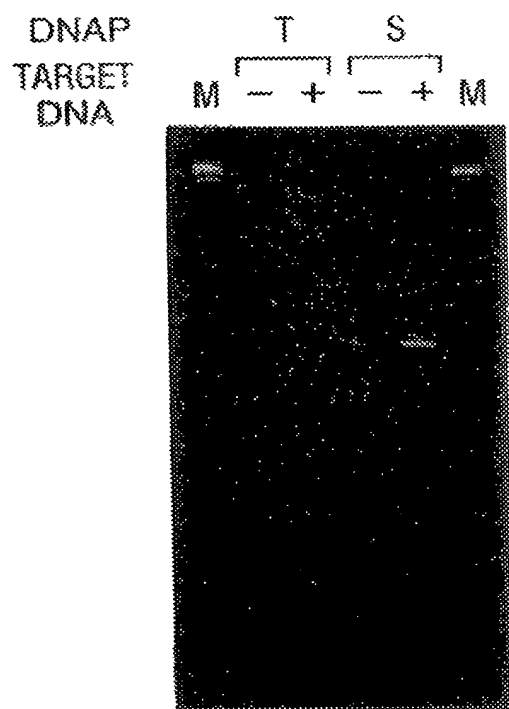


FIG. 7

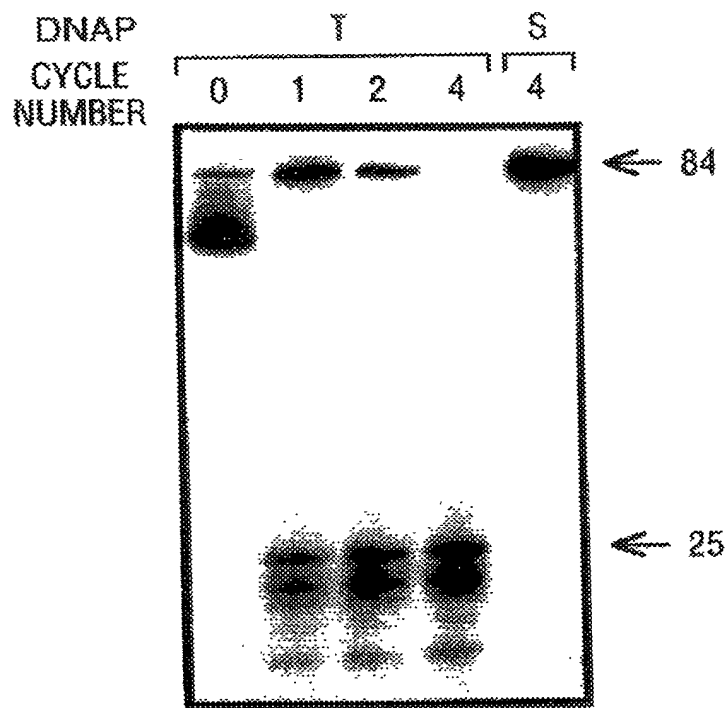


FIG. 8

	1	2	3	4	5	6
DNAP-T:	-	+	+	+	+	+
MgCl ₂ :	+	-	+	+	+	+
dNTPs:	+	-	+	-	+	-
Primers:	+	-	+	+	-	-

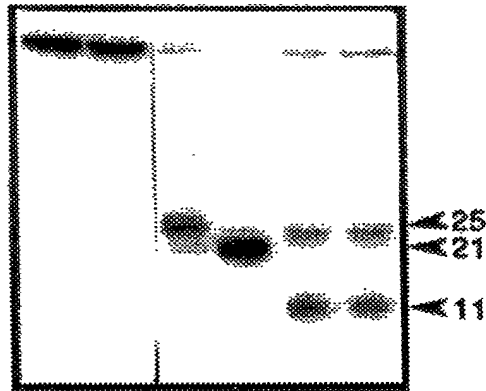


FIG. 9A

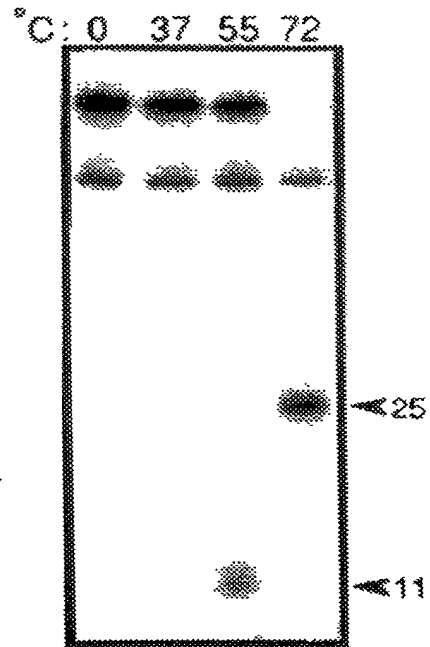


FIG. 9B

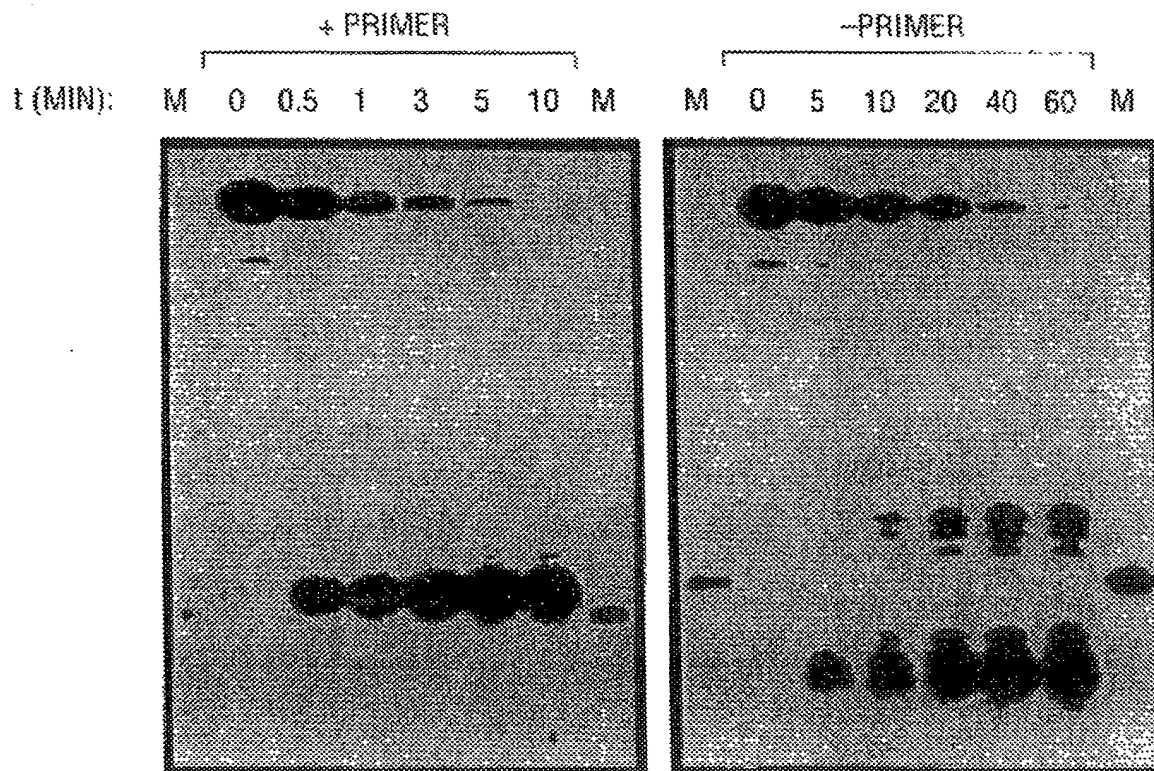


FIG. 10A

FIG. 10B

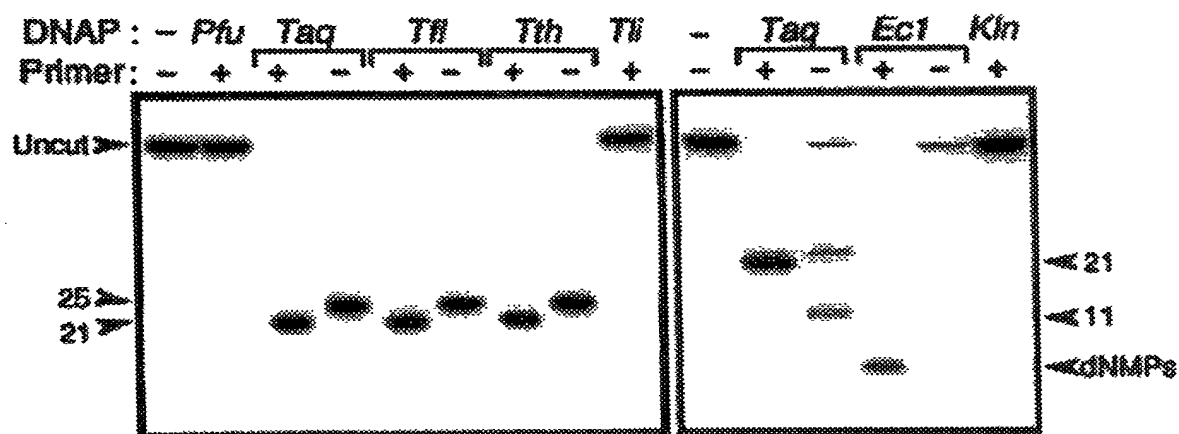
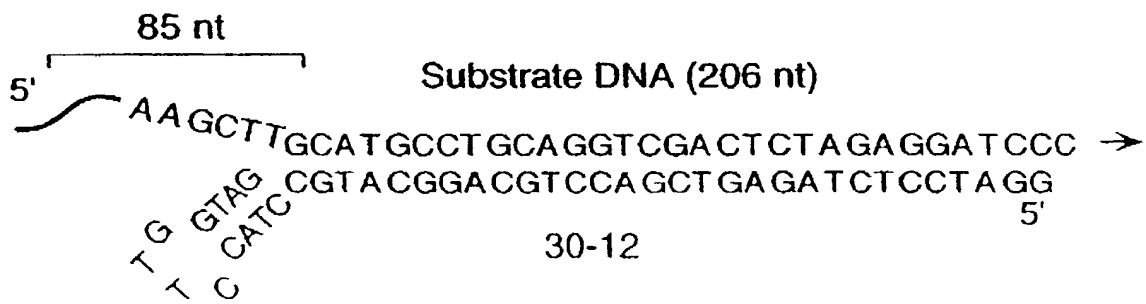
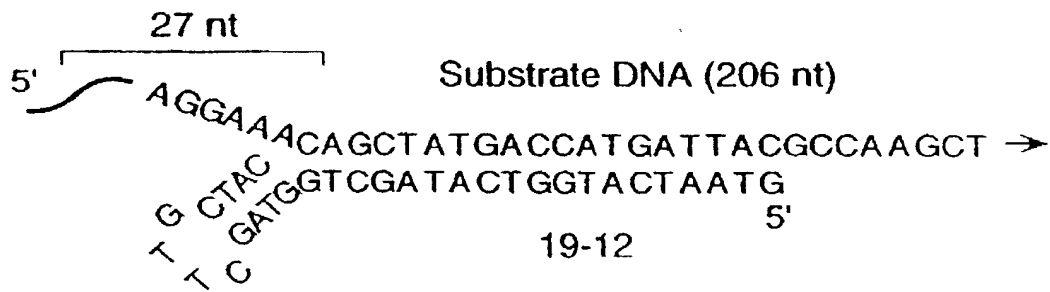


FIG. 12A



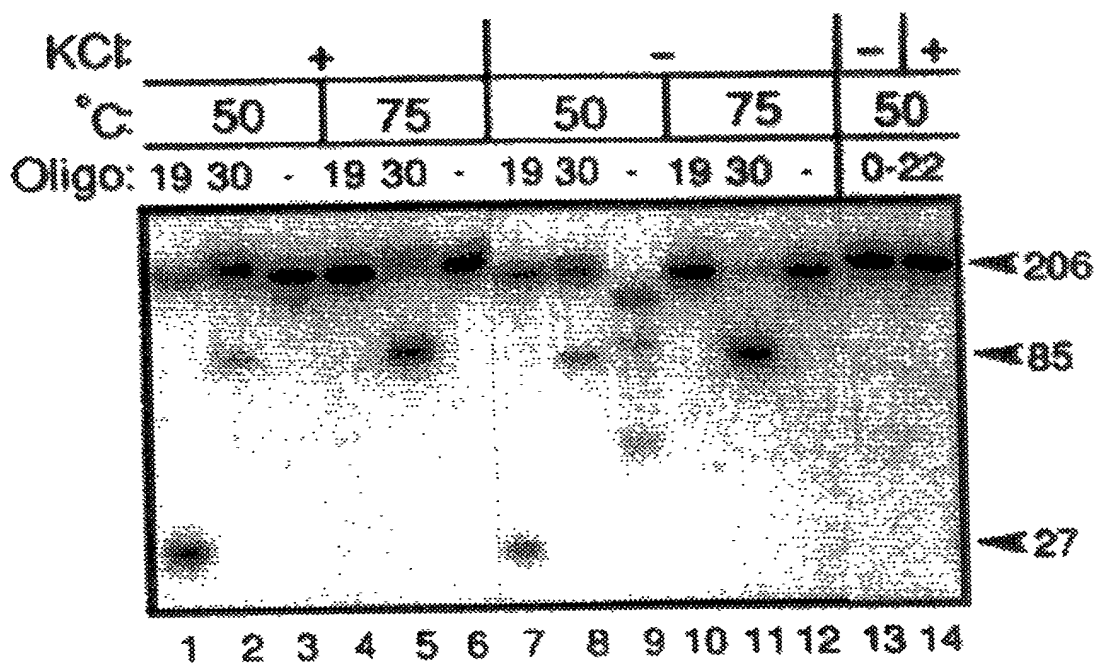


FIG. 12B

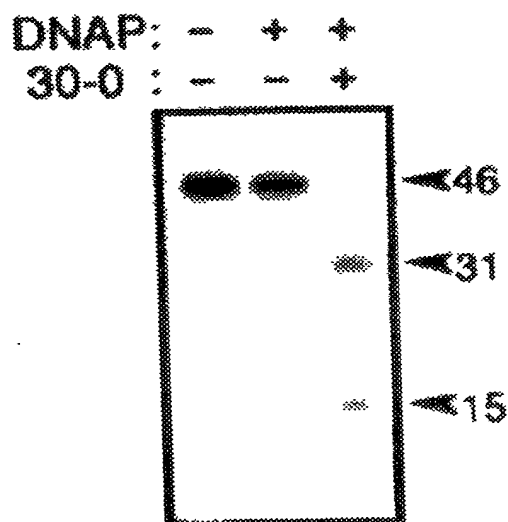


FIG. 13B

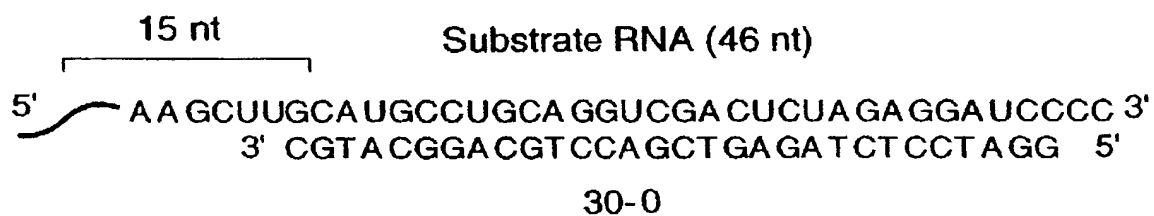


FIG. 13A

FIG. 14B

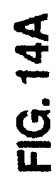
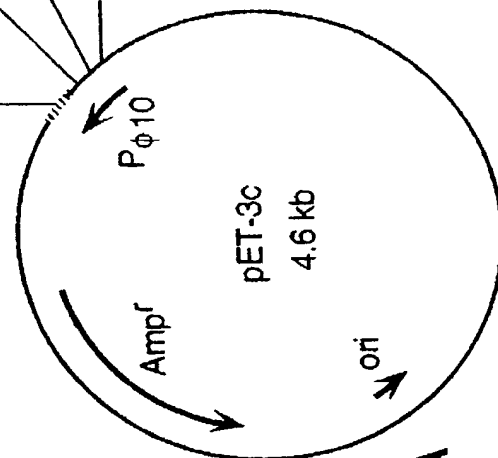
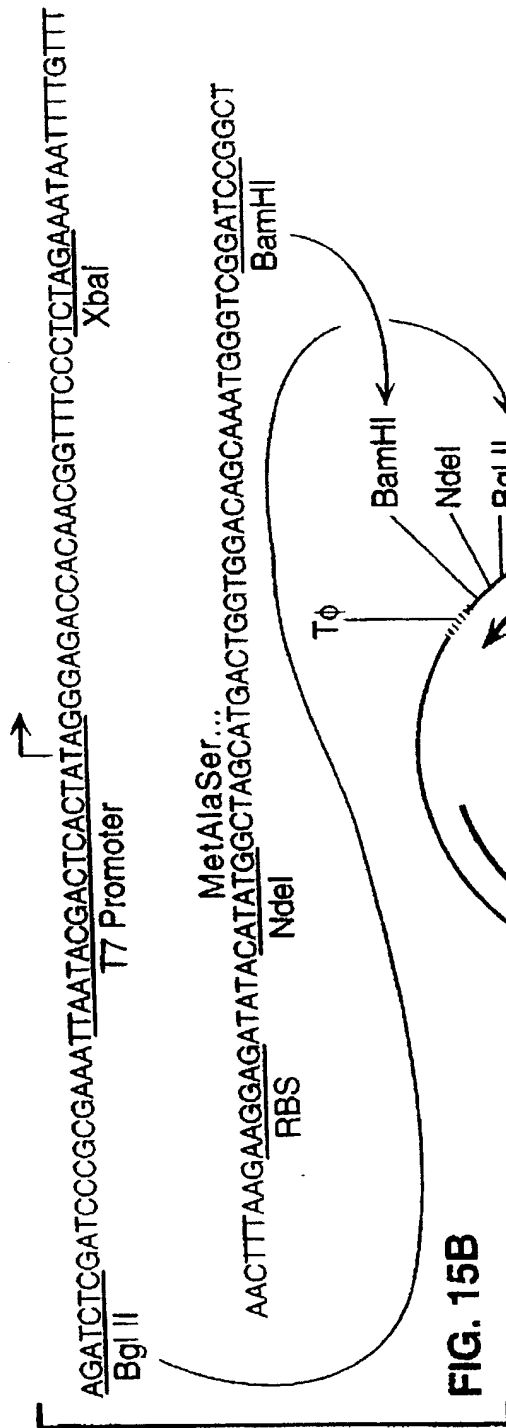


FIG. 14C



P_{φ10}: Bacteriophage T7 φ10 promoter

T_φ: T7 φ Terminator

RBS: Ribosome binding site

FIG. 15C

FIG. 16B

FIG. 16D

FIG. 16C

Diagram illustrating a DNA structure with a cleavage site and a primer. The DNA is shown as a double-stranded molecule. The top strand is labeled "5' arm" and contains the sequence: TAATACGACTCACTATAGGGAGAC. The bottom strand is labeled "3' arm" and contains the sequence: CTTAAGCTAATAATCGACTGTGATATCTTATGCT. A "Primer" is indicated by an arrow pointing to the sequence: CTTAAGCTAATAATCGACTGTGATATCTTATGCT. Two cleavage sites are marked with arrows labeled "a" and "b". Site "a" is located at the junction of the 5' arm and the 3' arm, specifically at the GAGAC sequence. Site "b" is located on the 3' arm, specifically at the GAGAC sequence. The label "Cleavage Sites" is positioned above the arrows.

FIG. 16E

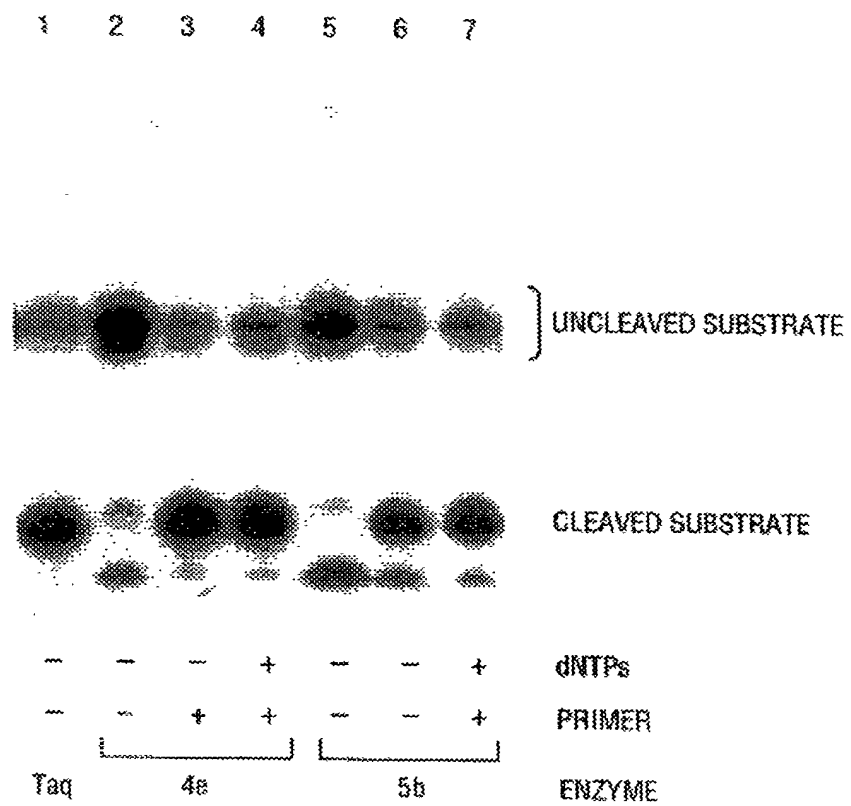


FIG. 17

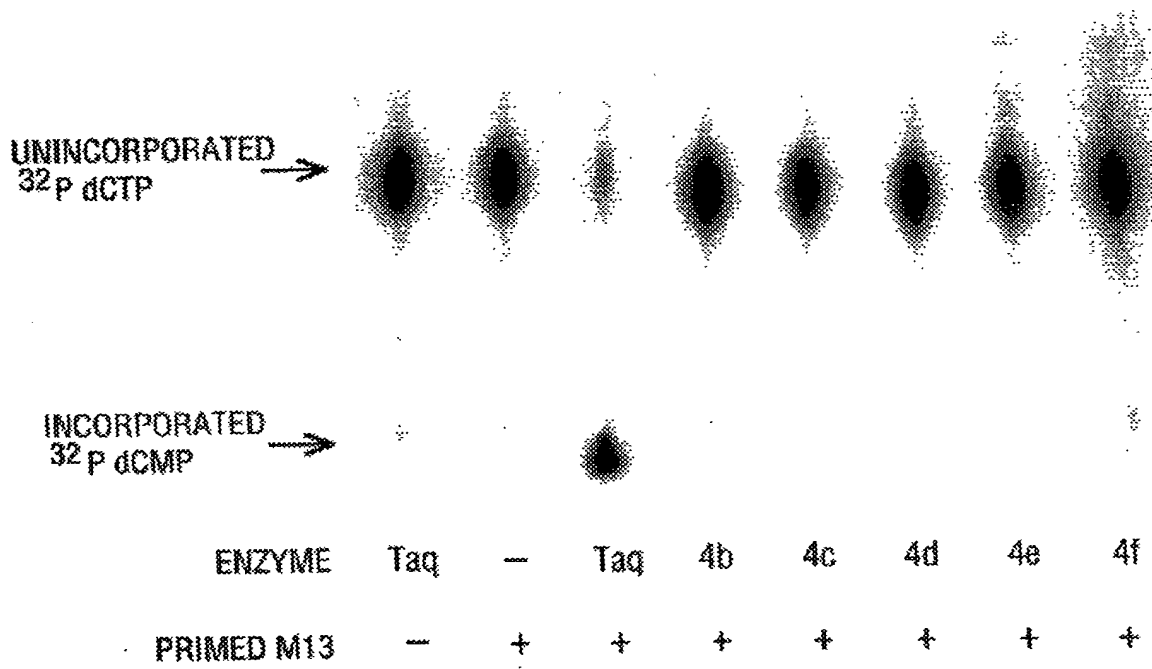


FIG. 18

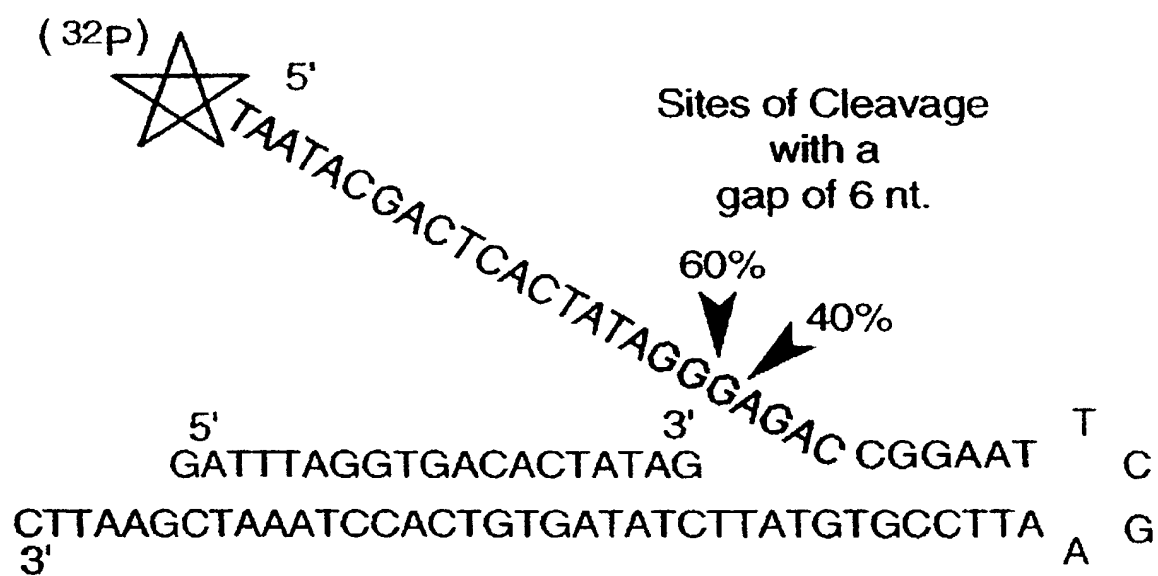
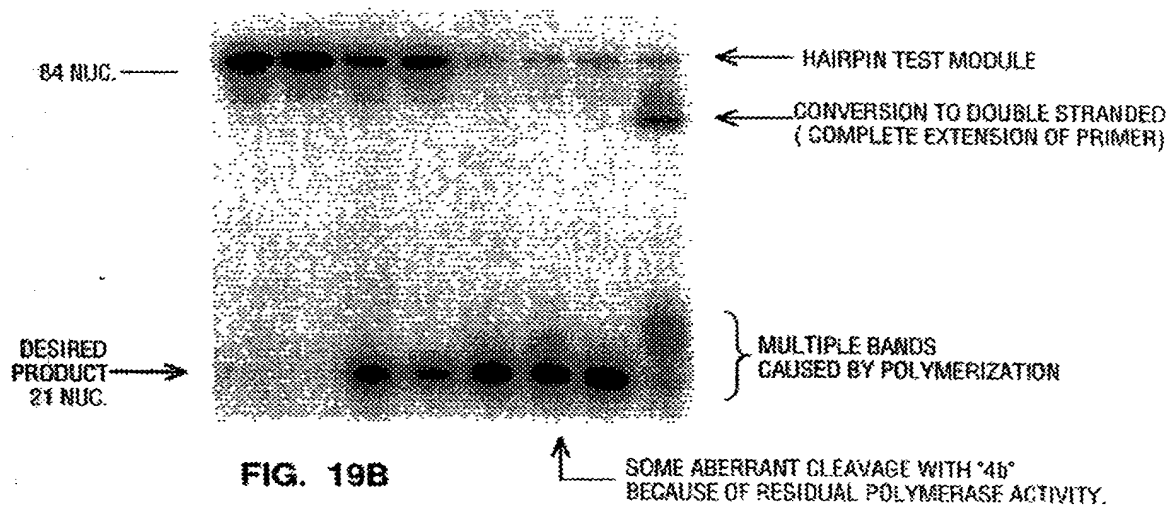


FIG. 19A

		4d		*4b*		UNMODIFIED	
		NO POL. ACTIVITY		2 PT. MUTATION SMALL ACTIVITY		DNAP Tag	
1	2	3	4	5	6	7	8
		-	+	-	+	-	+

dNTP



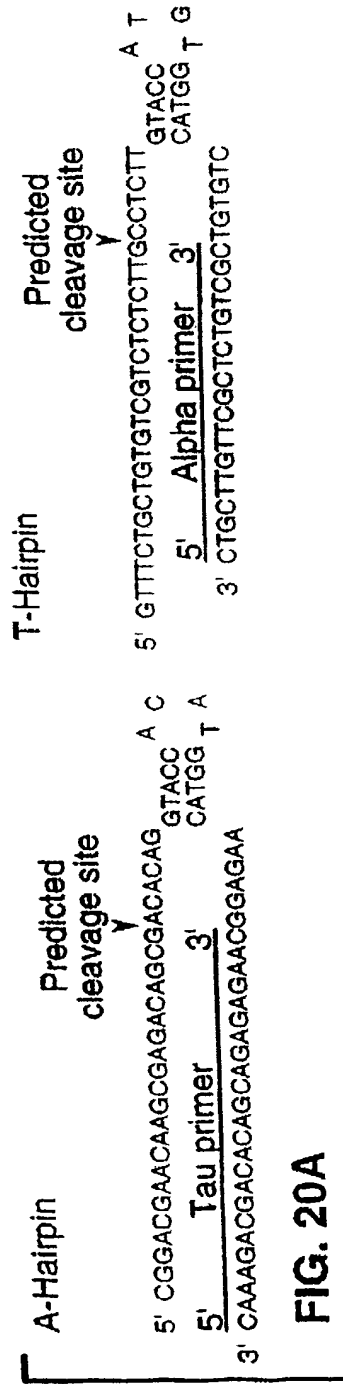


FIG. 20A

Sequence of alpha primer:

5' GACGAACAAGCGAGACAGCG 3'

FIG. 20B

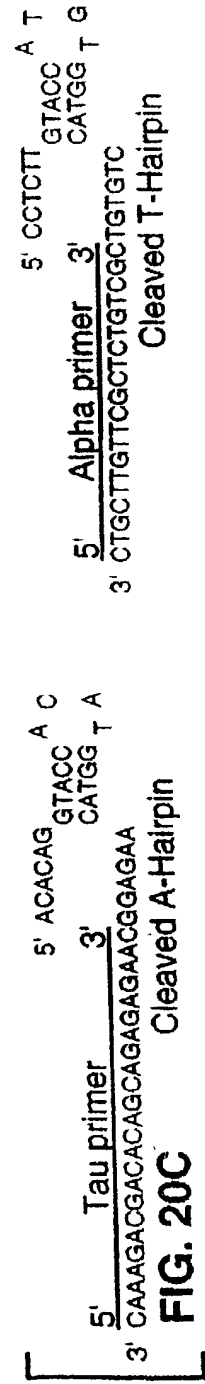


FIG. 20C

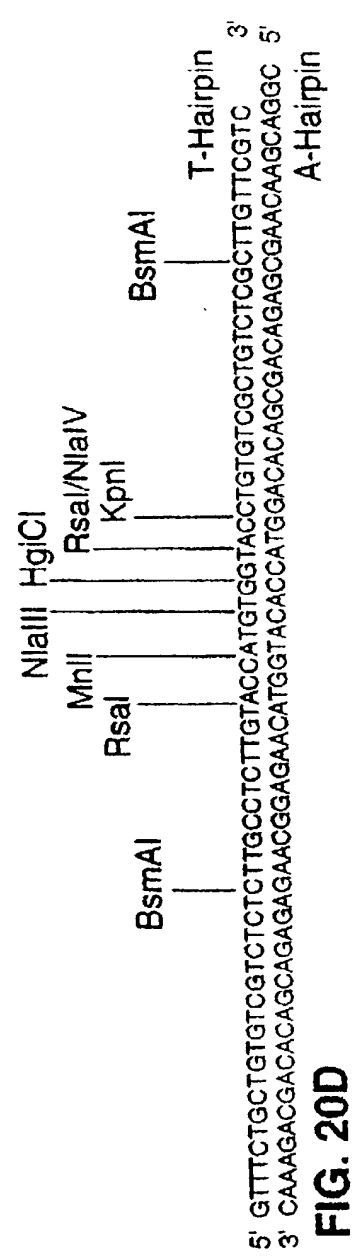


FIG. 20D

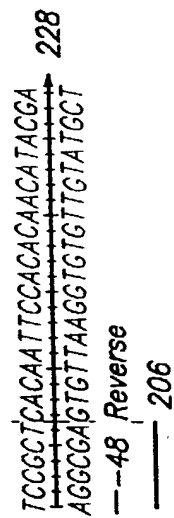
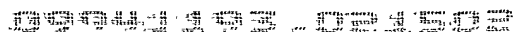


FIG. 21

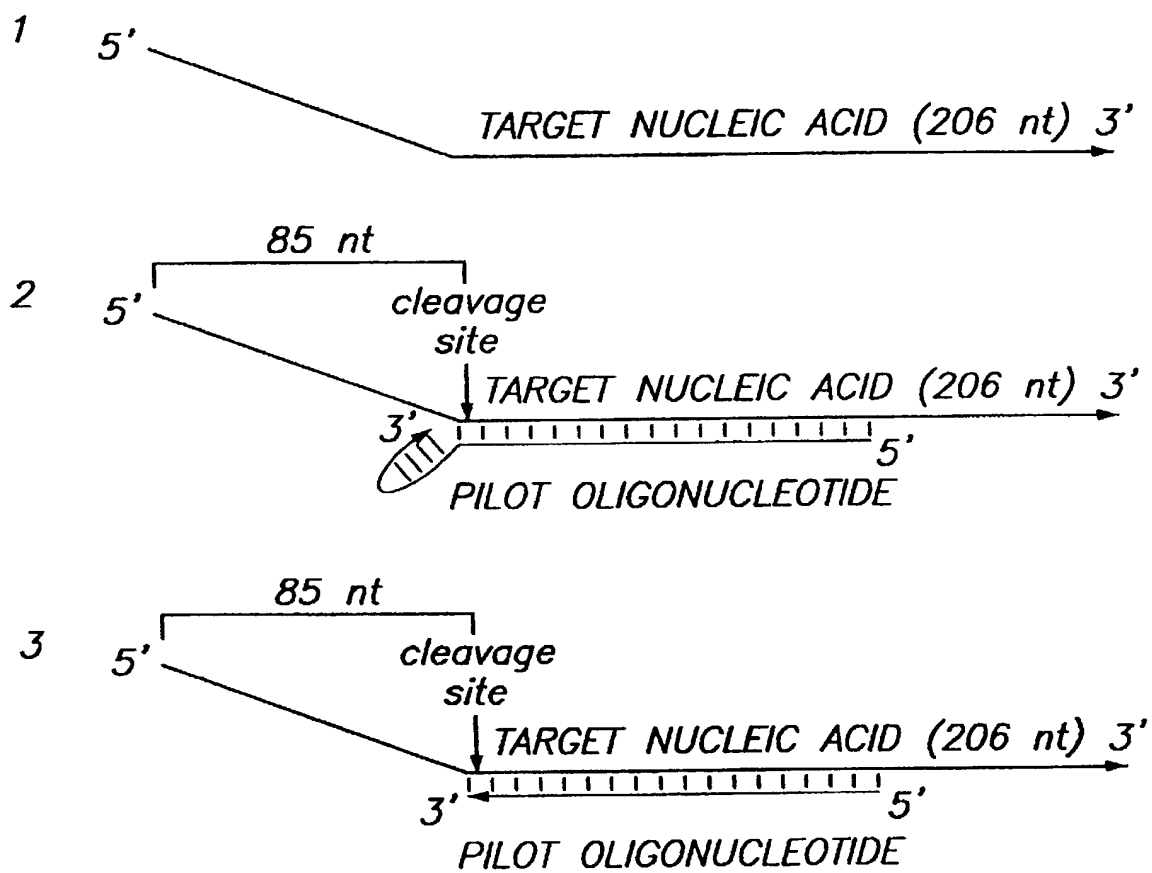


FIG. 22A

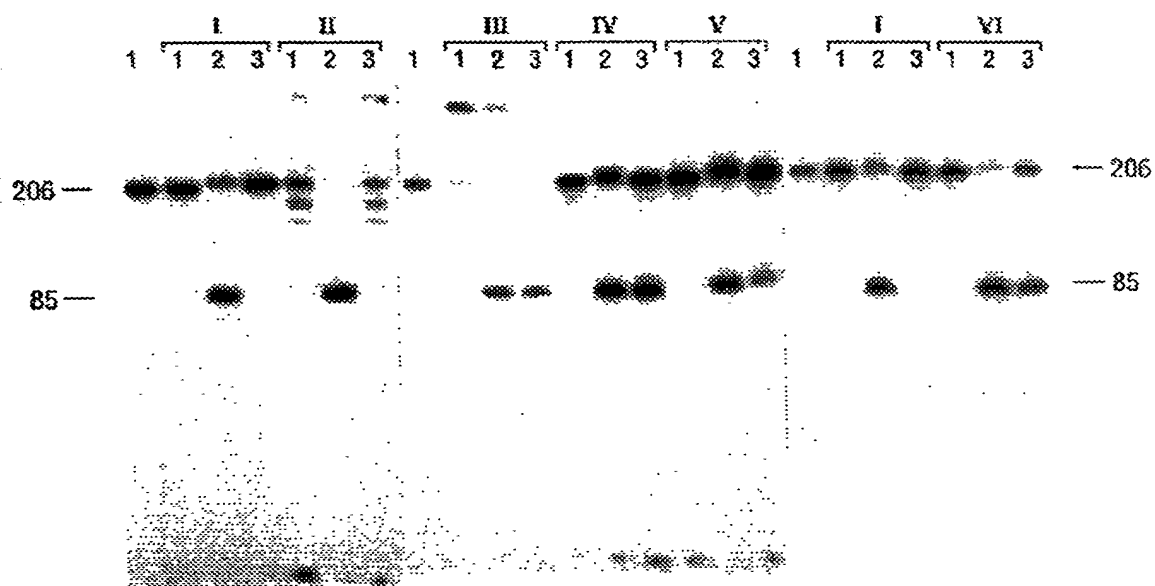


FIG. 22B

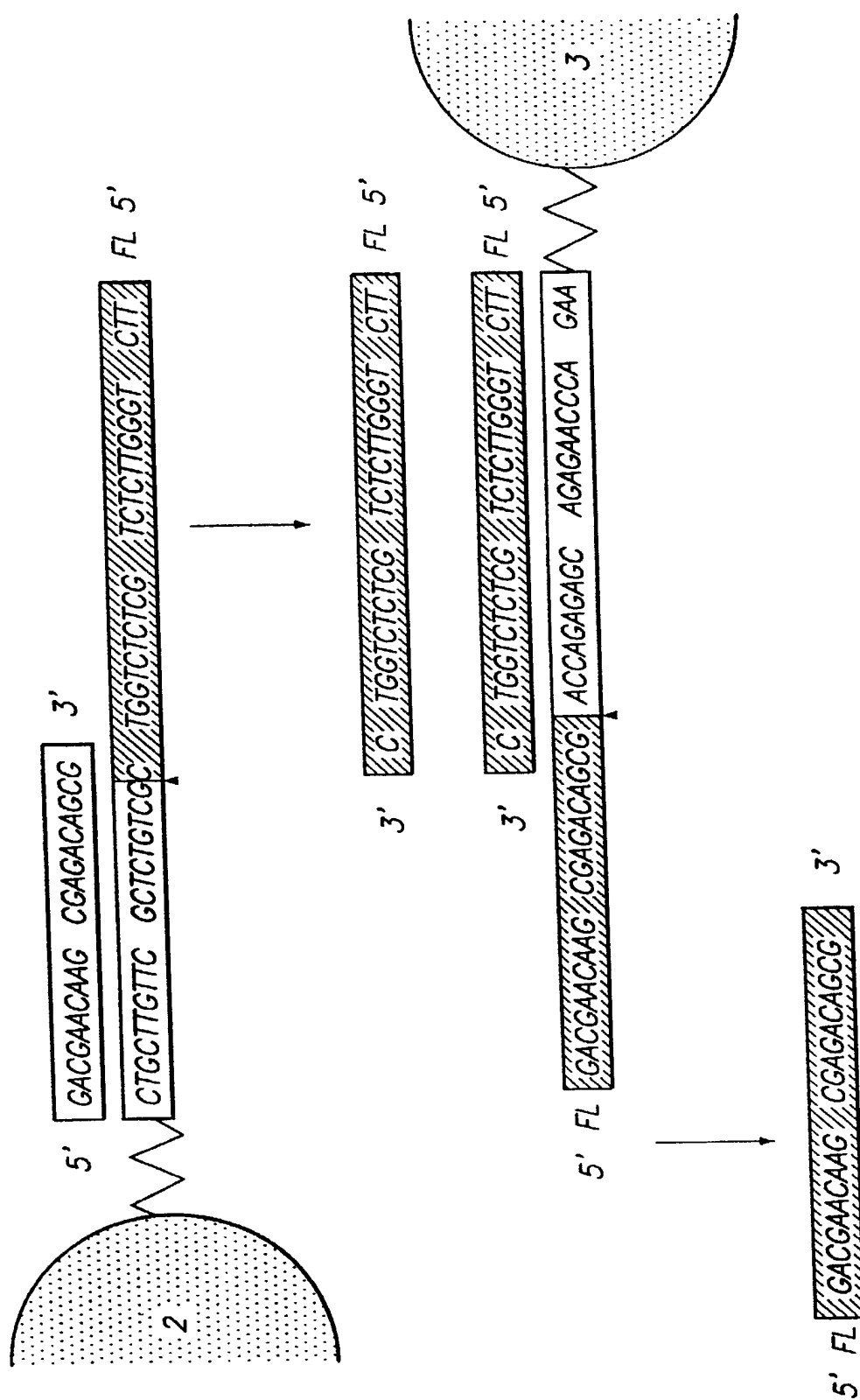


FIG. 23

[illegible]

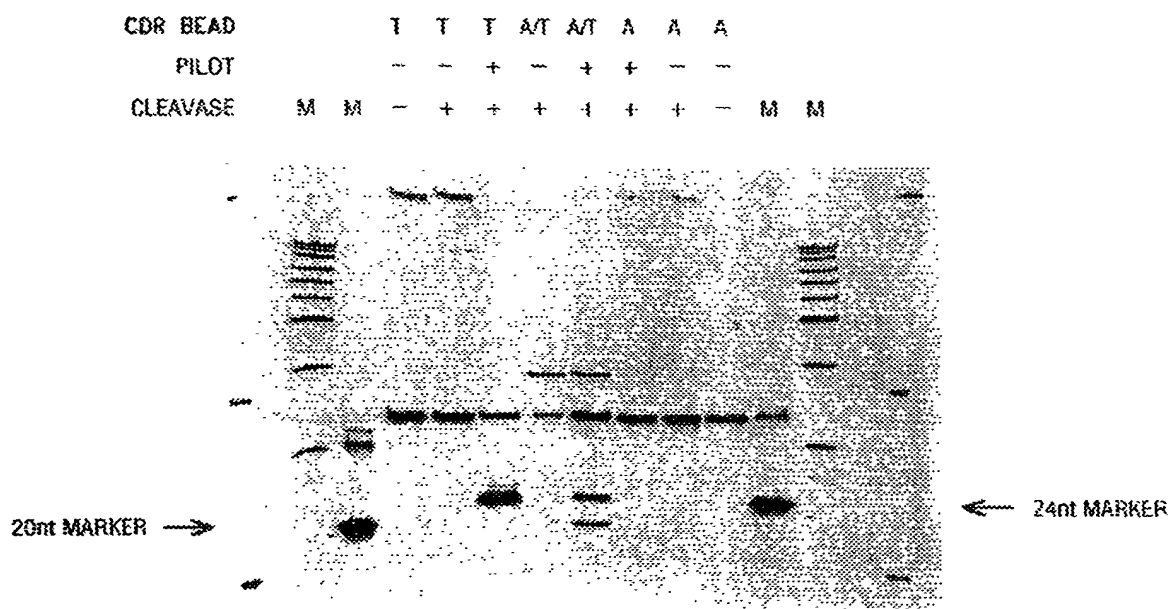


FIG. 24

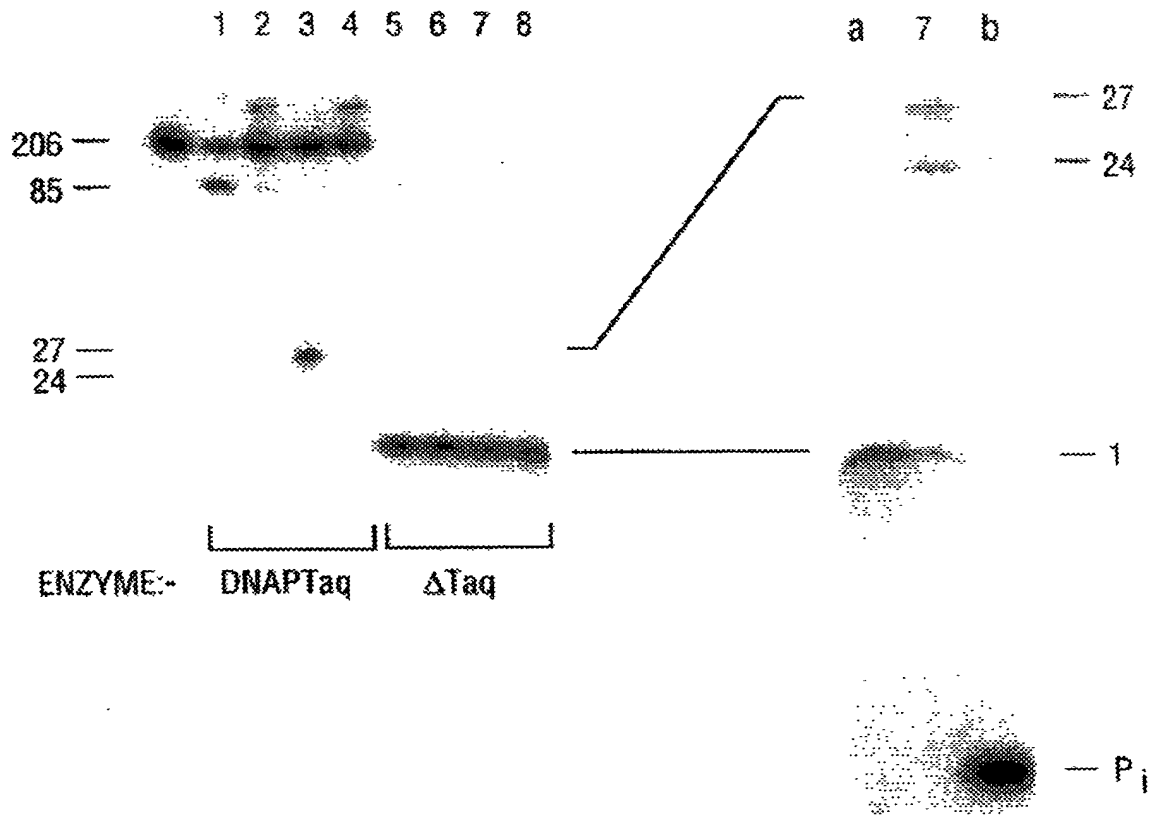


FIG. 25A

FIG. 25B

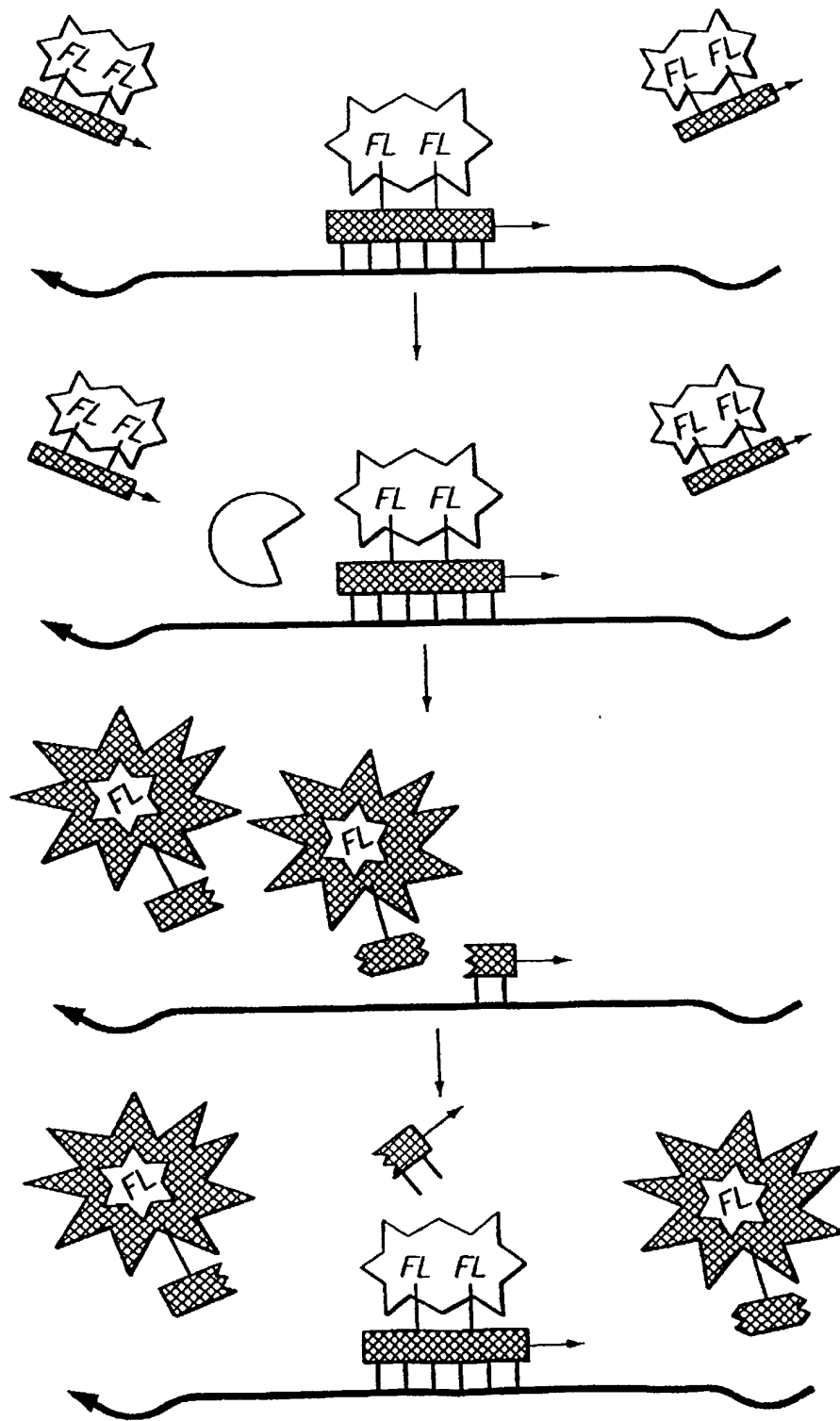


FIG. 27

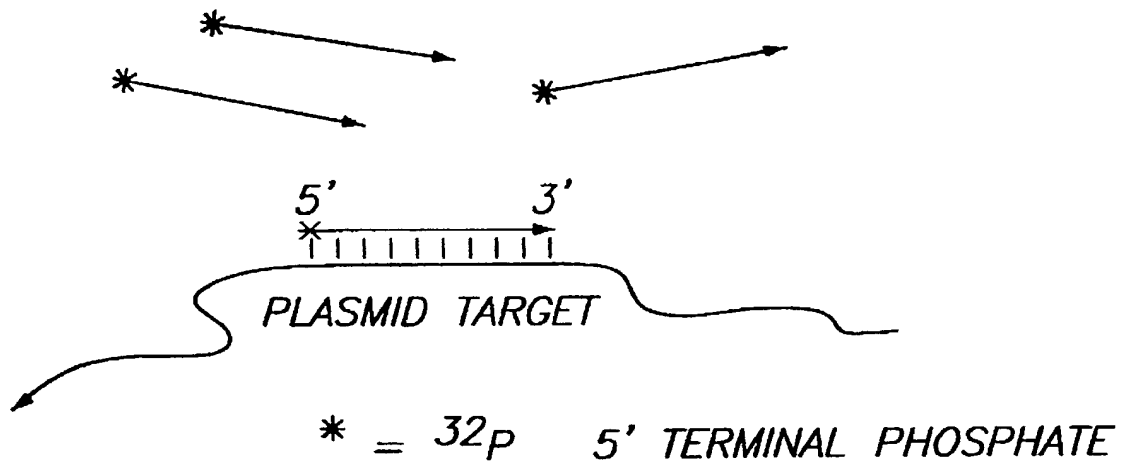


FIG. 28A

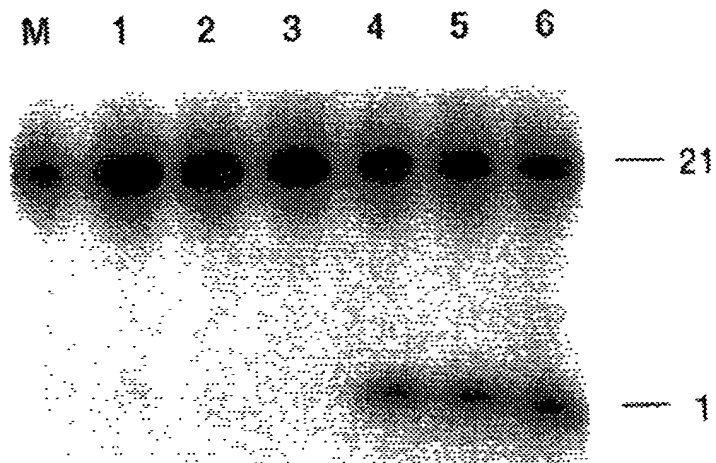


FIG. 28B

FIG. 29

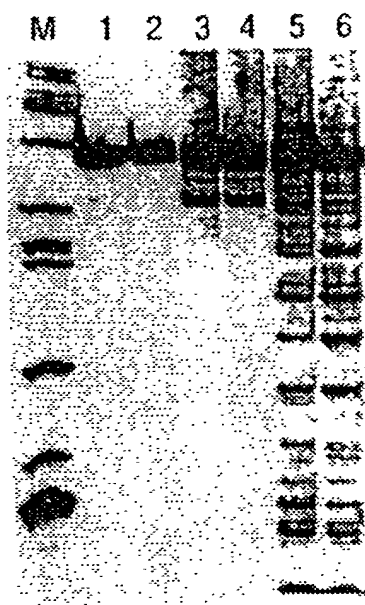


FIG. 30

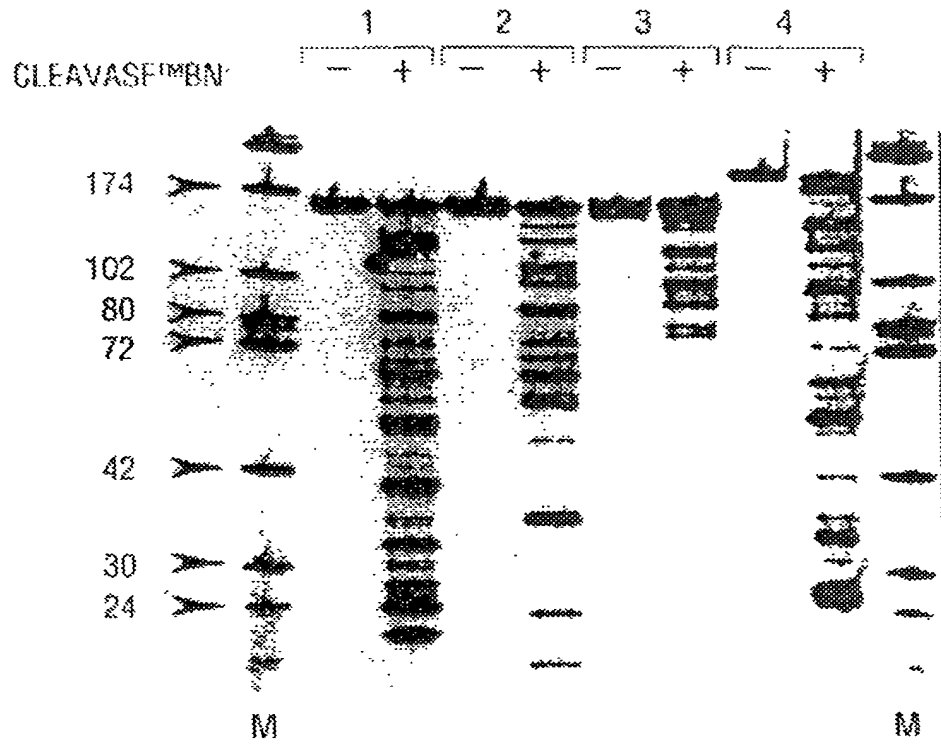


FIG. 31

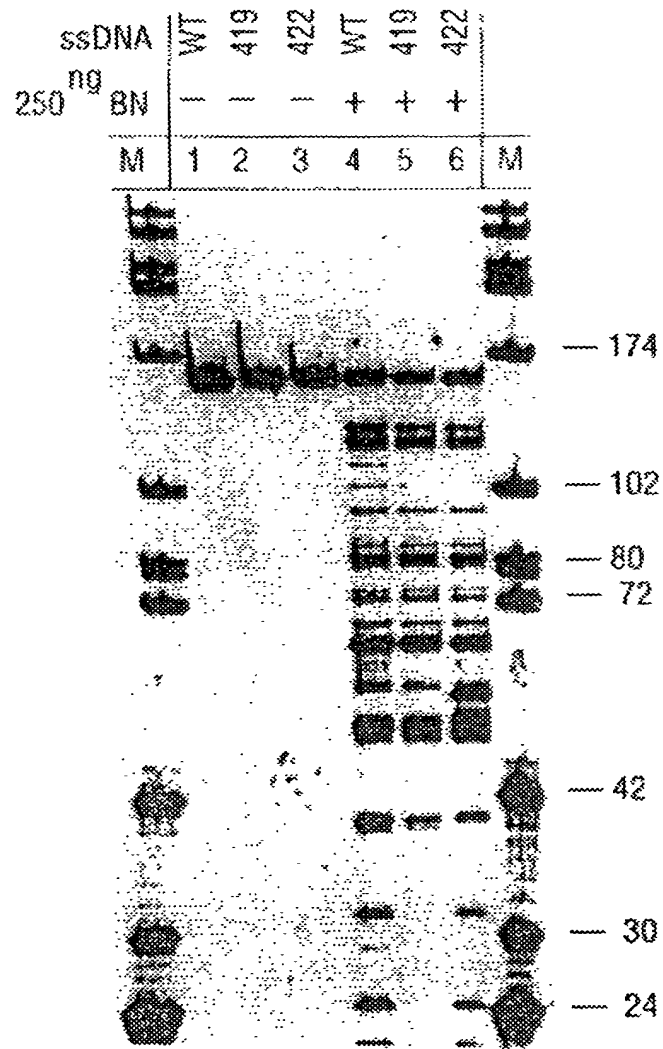


FIG. 32

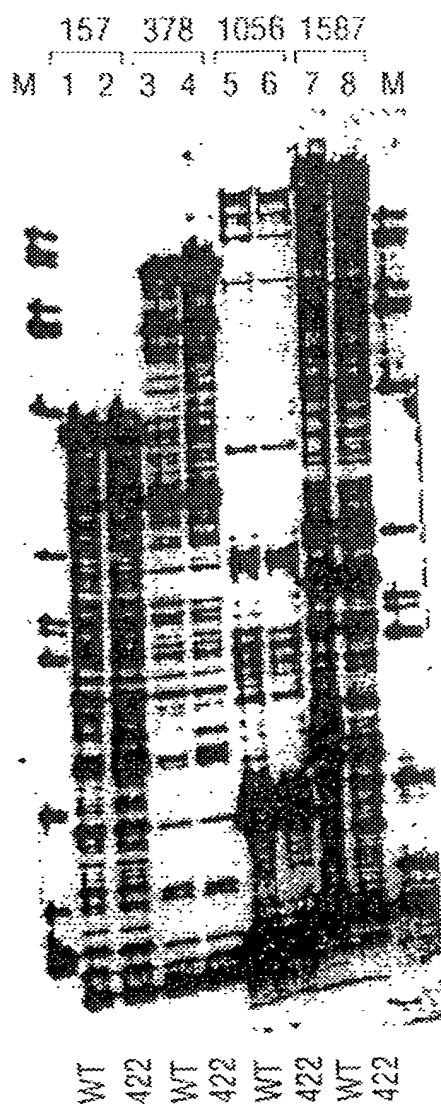


FIG. 33

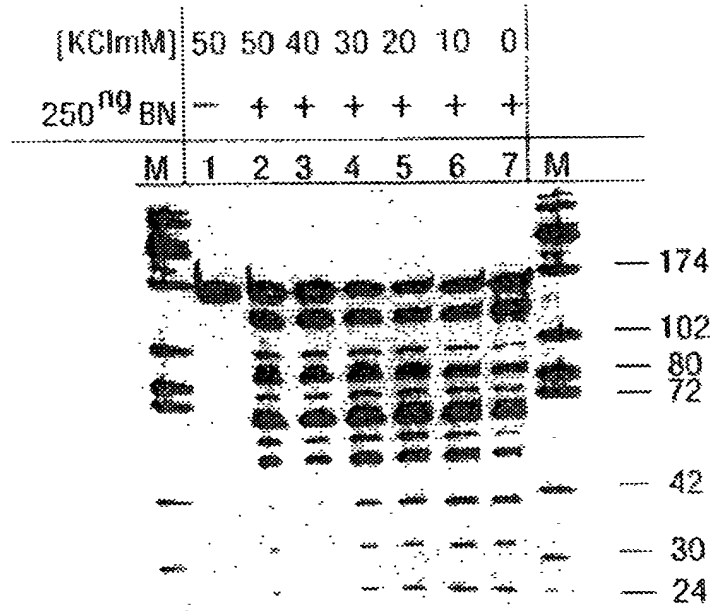


FIG. 35

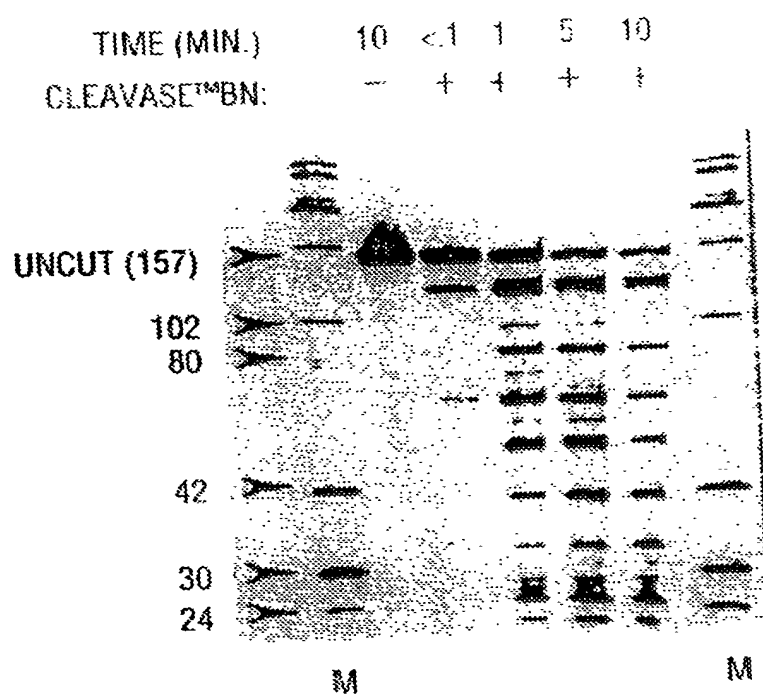


FIG. 36

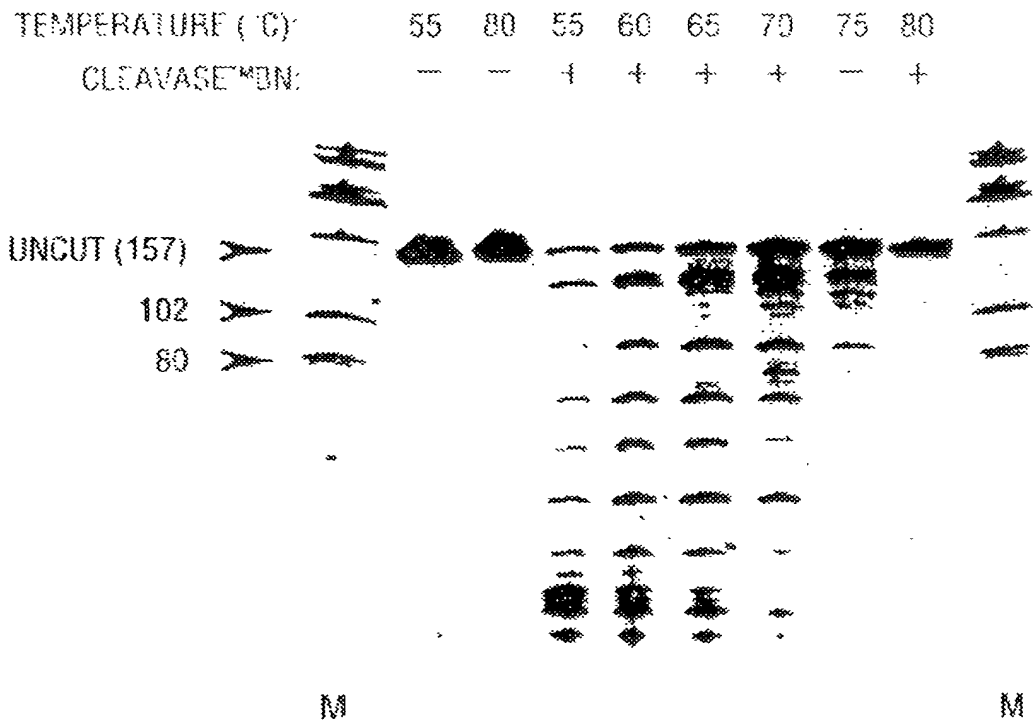


FIG. 37

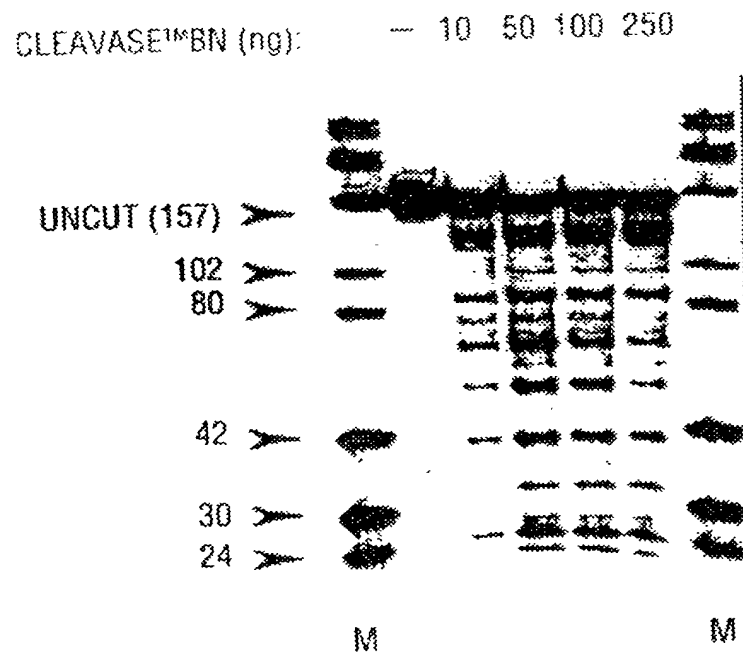


FIG. 38

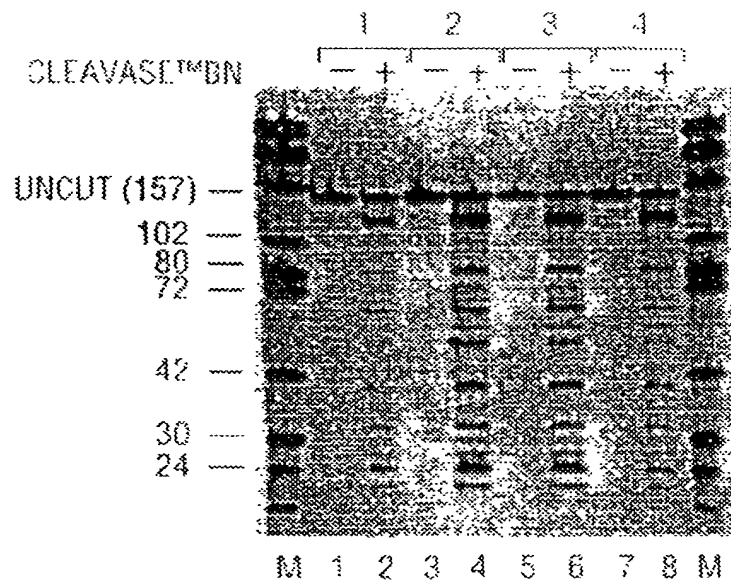


FIG. 39

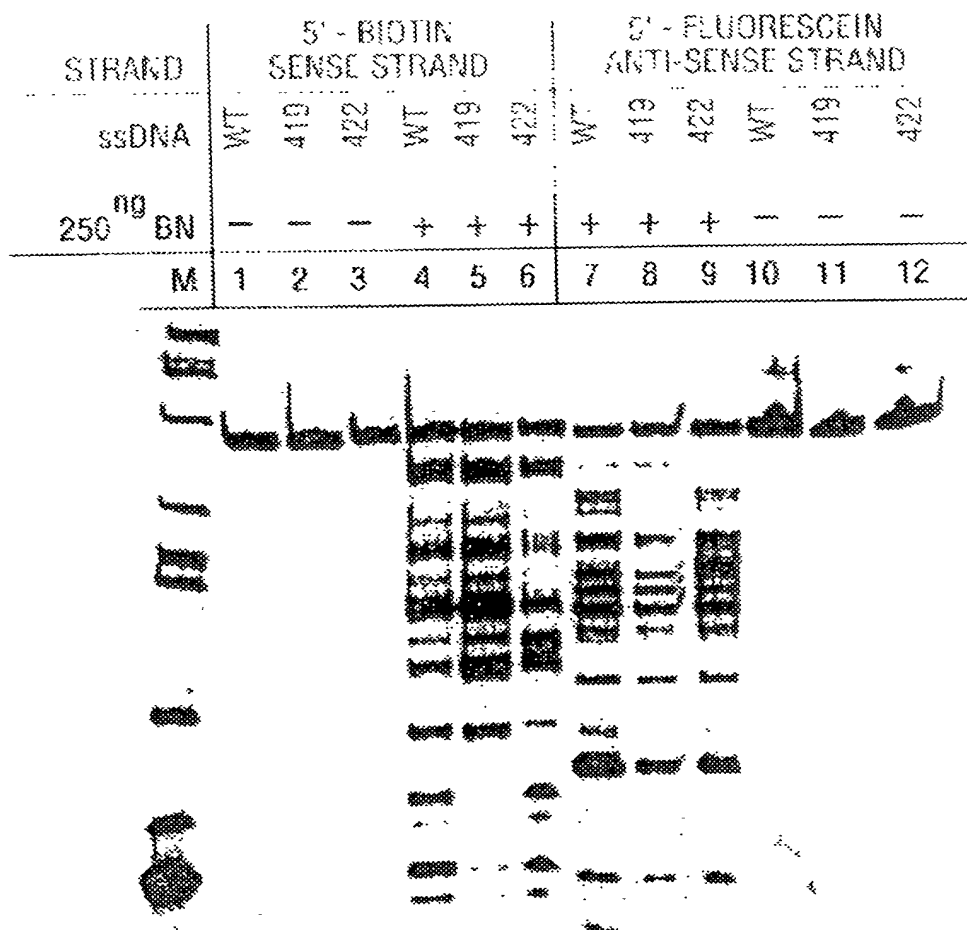


FIG. 40

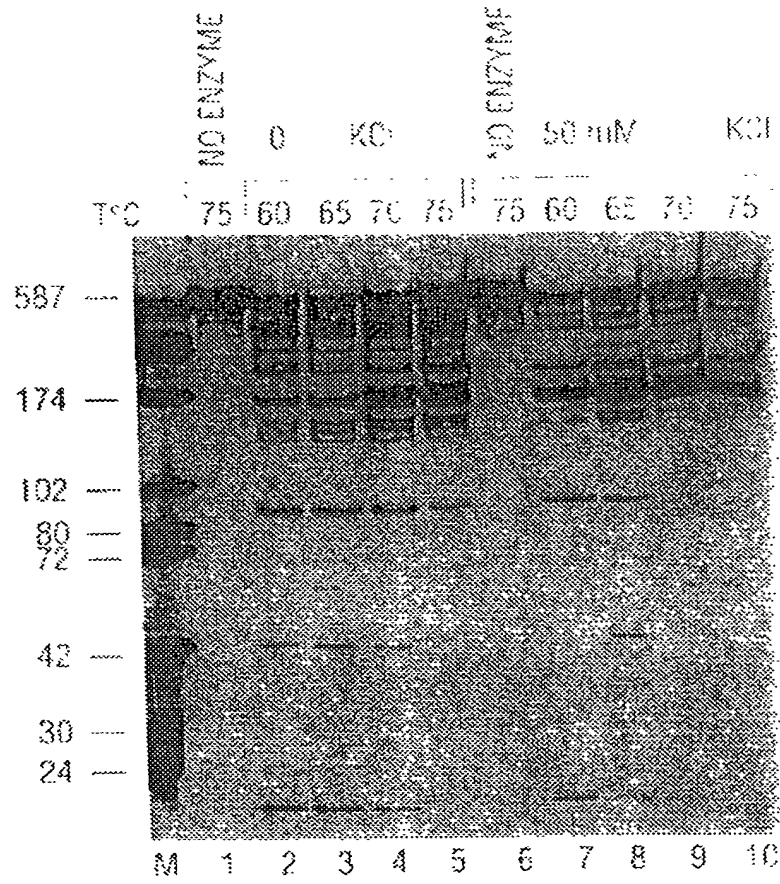


FIG. 41

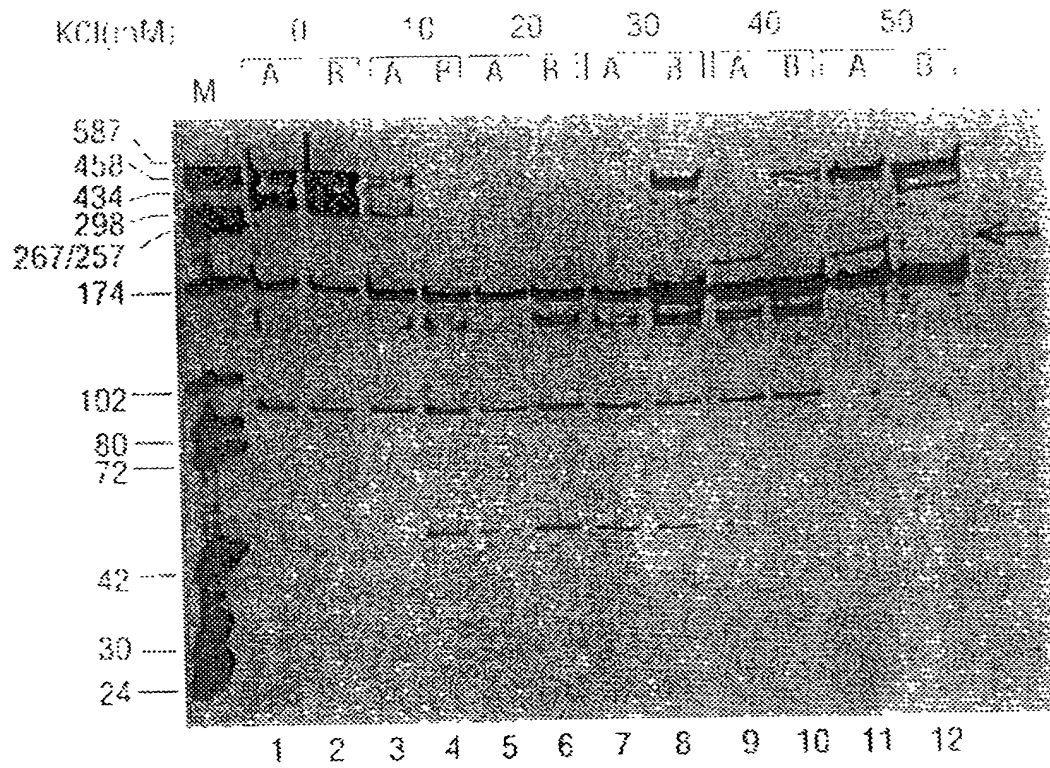


FIG. 42

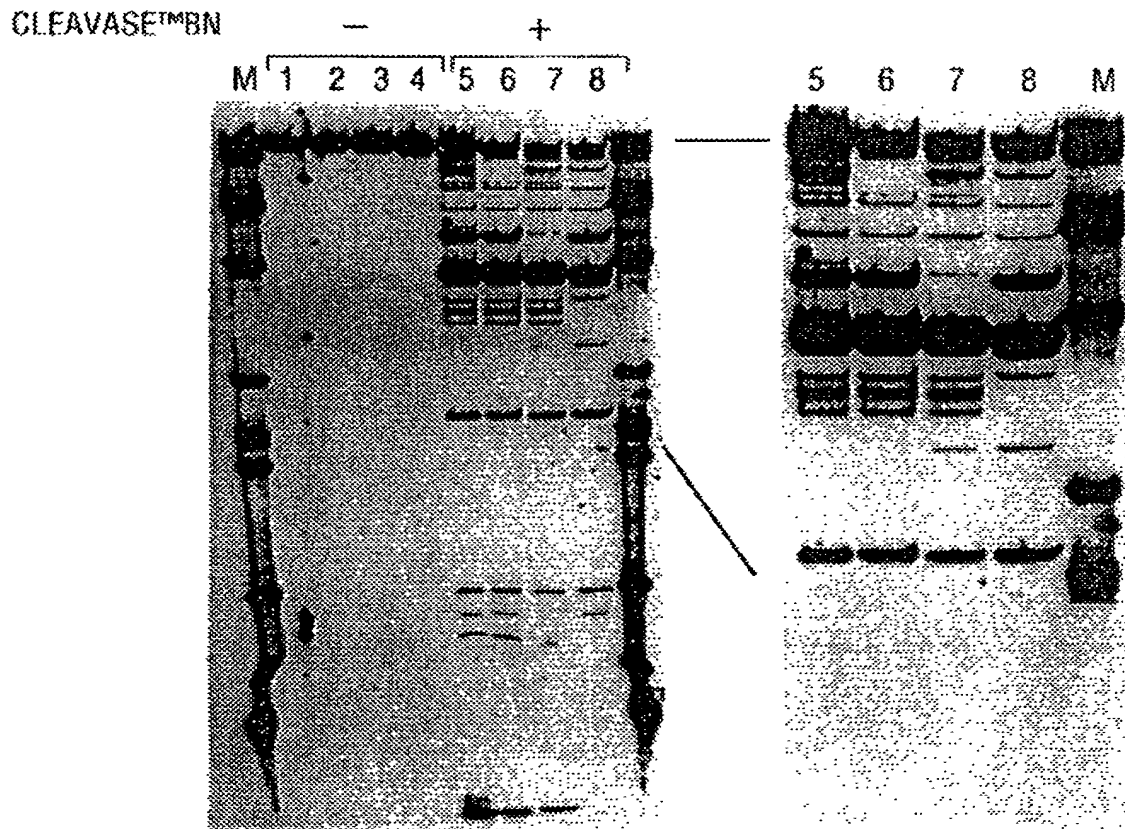


FIG. 43

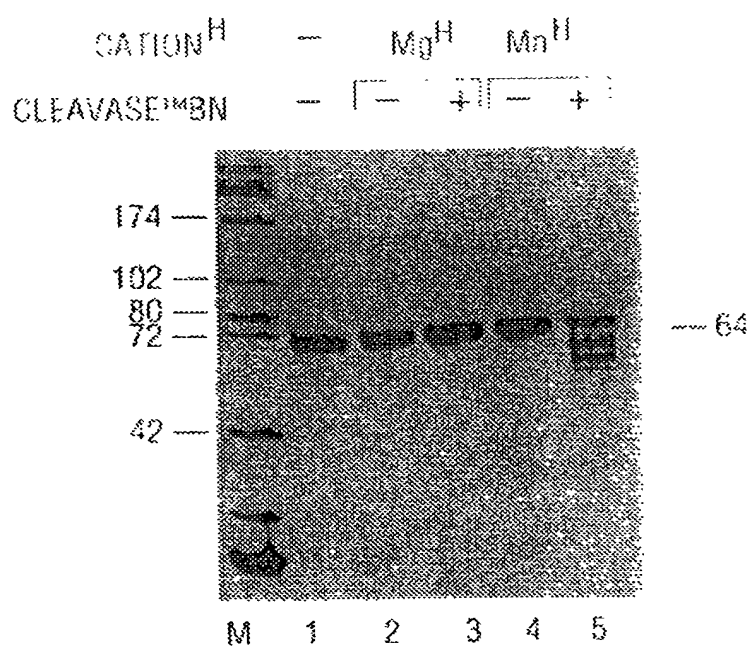


FIG. 44

BN 1AQ

WT 422 WT 422

M 1 2 3 4 M

FIG. 45

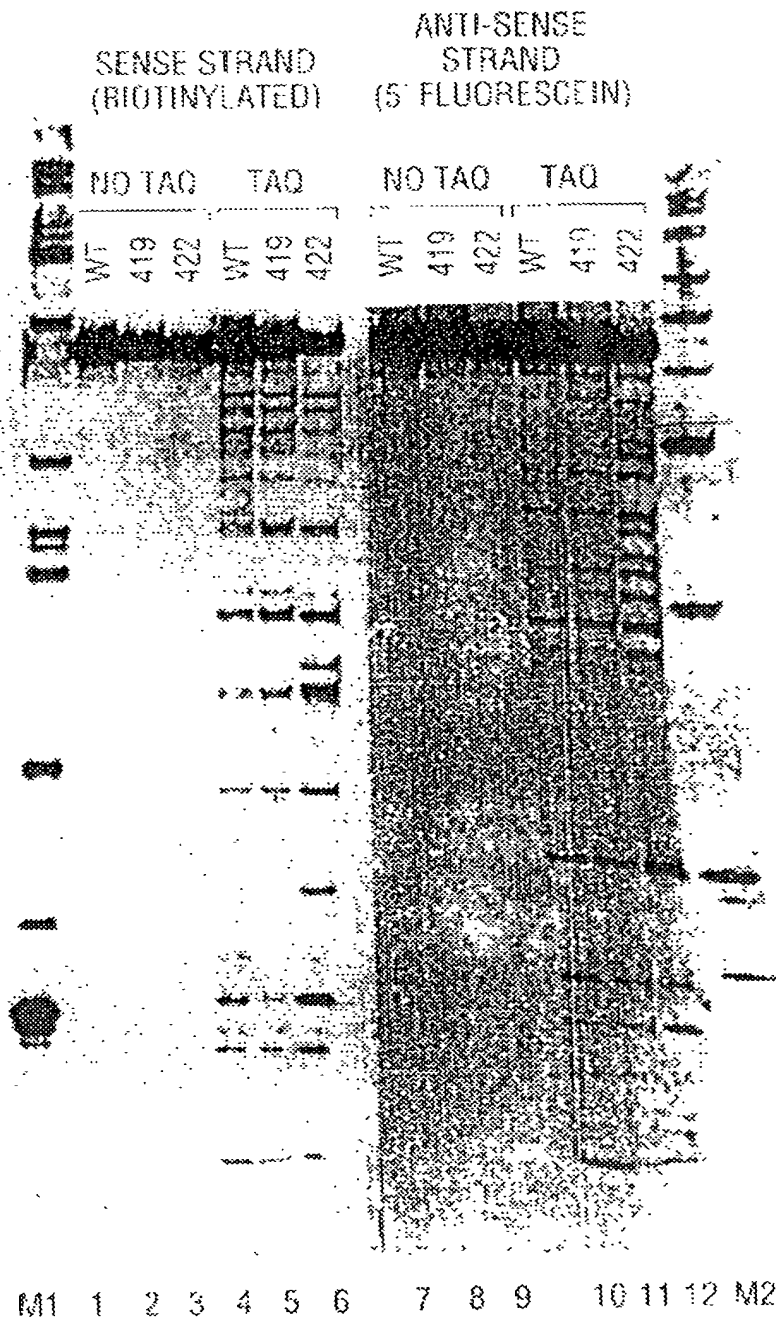


FIG. 46

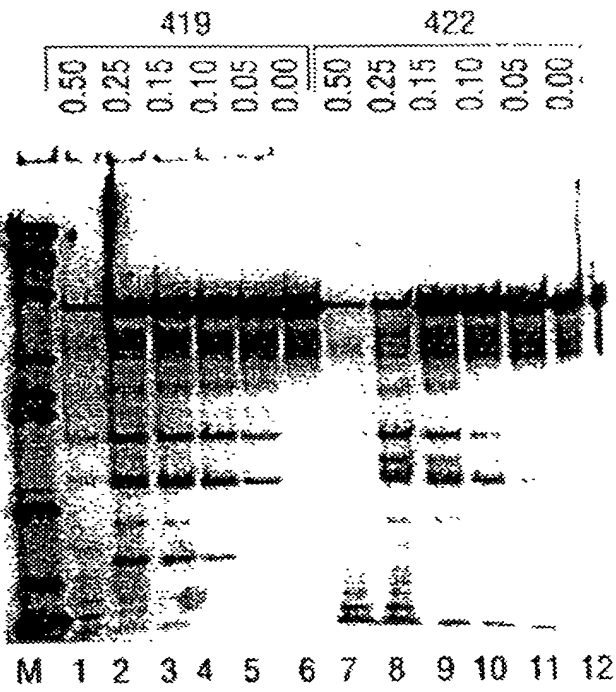


FIG. 47

WILD TYPE
R422Q

L.100.8-1
(SEQ ID NO: 76) 5'GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGGACTTTCCACAAGGGG
3'CCGACTGTTCTTCCCTTGAGCGACTCTGTCGTCCCTGAAAGGTGTTCCCC

L.46.16-10
(SEQ ID NO: 77) 5'GGCTGACAAGAAGGAAACTCGCTGAGATAGCAGGGGACTTTCCACAAGGGG
3'CCGACTGTTCTTCCCTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC

L.46.16-12
(SEQ ID NO: 78) 5'GGCTGACAAGAAGGAAACTCGCTGAGATAGCAGGGGACTTTCCACAAGGGG
3'CCGACTGTTCTTCCCTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC

L19.16-3
(SEQ ID NO: 79) 5'GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGGACTTTCCACAAGGGG
3'CCGACTGTTCTTCCCTTGAGCGACTCTGTCGTCCCTGAAAGGTGTTCCCC

L.CEM/251
(SEQ ID NO: 80) 5'GGCTGACAAGAAGGAAACTCGCTGAAACAGCAGGGGACTTTCCACAAGGGG
3'CCGACTGTTCTTCCCTTGAGCGACTTTGTCGTCCCTGAAAGGTGTTCCCC

L.36.8-3
(SEQ ID NO: 81) 5'GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGGACTTTCCACAAGGGG
3'CCGACTGTTCTTCCCTTGAGCGACTCTGTCGTCCCTGAAAGGTGTTCCCC

FIG. 49A

CGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGGACTTTCCACAAGGGG

150

L.100.8-1
 5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCGGA
 3'ACTACATATTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCT

L.46.16-10
 5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCGGA
 3'ACTACATATTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCT

L.46.16-12
 5'TGGTGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCGGA
 3'ACCACATATTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCT

L.19.16-3
 5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCGGA
 3'ACTACATATTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCT

L.CEM/251
 5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCGGA
 3'ACTACATATTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCT

L.36.8-3
 5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCGGA
 3'ACTACATATTTATAGTGACGTAAGCGAGACATAAGTCAGCGAGACGCCT

FIG. 49C

CGCGAGACGCTCTGCGGATTCAGTCGCTCTGTATTTCAGTCGCTCTGCGGA

L.100.8-1	<p>GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC</p>	200
L.46.16-10	<p>GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC</p>	
L.46.16-12	<p>GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC</p>	
L.19.16-3	<p>GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC</p>	
L.CEM/251	<p>GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC</p>	
L.36.8-3	<p>GAGGCTGGCAGATTGAGCCCTAGGAGGTTCTCTCCAGCACTAGCAGGTAG CTCCGACCGTCTAACTCGGGATCCTCCAAGAGAGGTCGTGATCGTCCATC</p>	

FIG. 49D

200 199 198 197 196 195 194 193 192 191 190 189 188 187 186 185 184 183 182 181 180 179 178 177 176 175 174 173 172 171 170 169 168 167 166 165 164 163 162 161 160 159 158 157 156 155 154 153 152 151 150 149 148 147 146 145 144 143 142 141 140 139 138 137 136 135 134 133 132 131 130 129 128 127 126 125 124 123 122 121 120 119 118 117 116 115 114 113 112 111 110 109 108 107 106 105 104 103 102 101 100 99 98 97 96 95 94 93 92 91 90 89 88 87 86 85 84 83 82 81 80 79 78 77 76 75 74 73 72 71 70 69 68 67 66 65 64 63 62 61 60 59 58 57 56 55 54 53 52 51 50 49 48 47 46 45 44 43 42 41 40 39 38 37 36 35 34 33 32 31 30 29 28 27 26 25 24 23 22 21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1

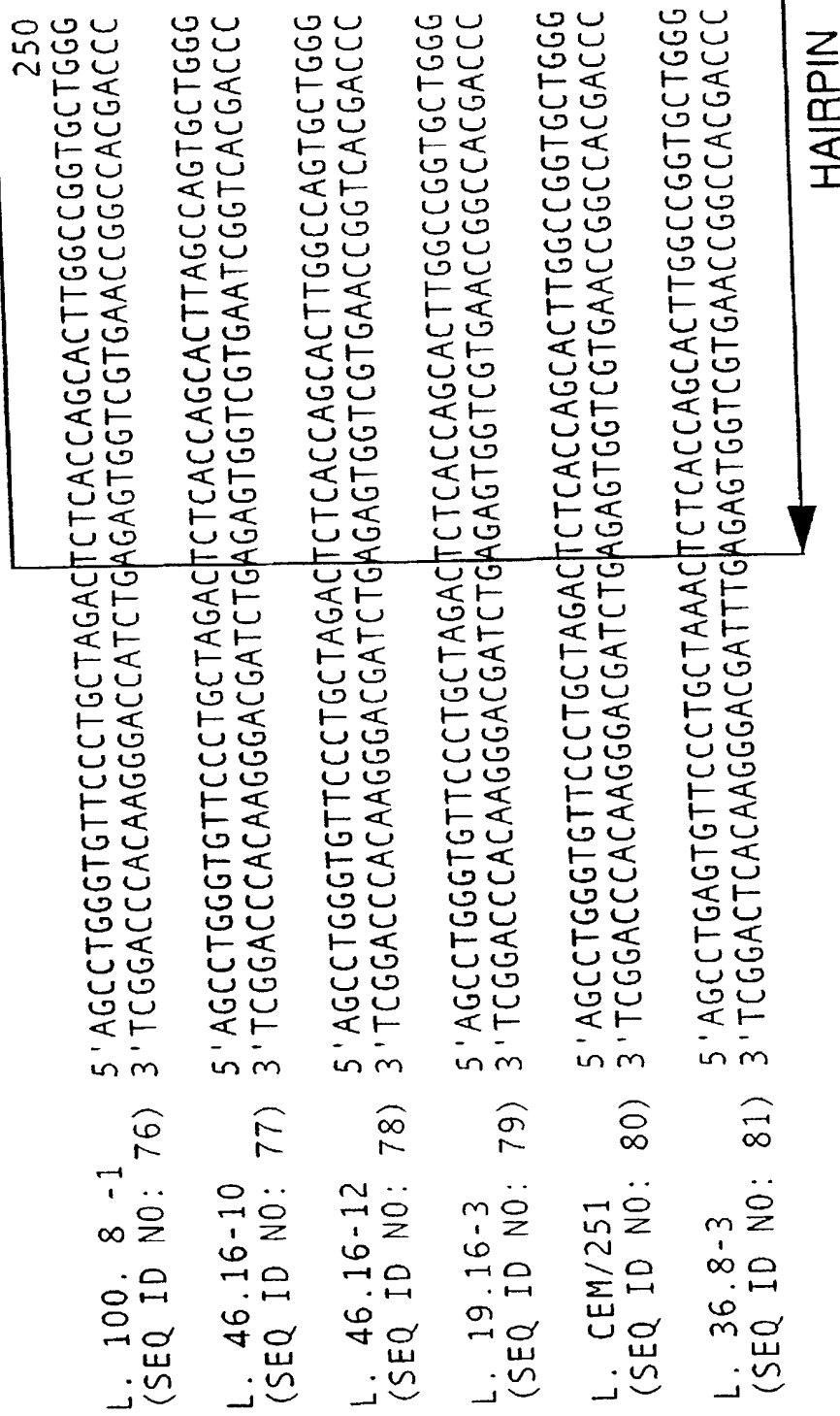


FIG. 49E

250 250 250 250 250 250 250 250

Accession	Sequence	Length
L.100.8-1	5'ATTTTAGAAGTAGGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG 3'TAAAATCTTCATCCGGTCACACACACAAAGGTAGAGGATCGGCGCGGAC	350 G 3' C 5'
L.46.16-10	5'ATTTTAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG 3'TAAAATCTTCATTCGGTCACACACACAAAGGTAGAGGATCGGCGCGGAC	G 3' C 5'
L.46.16-12	5'ATTTTAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG 3'TAAAATCTTCATTCGGTCACACACACAAAGGTAGAGGATCGGCGCGGAC	G 3' C 5'
L.19.16-3	5'ATTTTAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG 3'TAAAATCTTCATCCGATCACACACACAAAGGTAGAGGATCGGCGCGGAC	G 3' C 5'
L.CEM/251	5'ATTTTAGAAGTAAGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG 3'TAAAATCTTCATTCGATCACACACACAAAGGTAGAGGATCGGCGCGGAC	G 3' C 5'
L.36.8-3	5'ATTTTAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG 3'TAAAATCTTCATCCGATCACACACACAAAGGTAGAGGATCGGCGCGGAC	G 3' C 5'

FIG. 49G

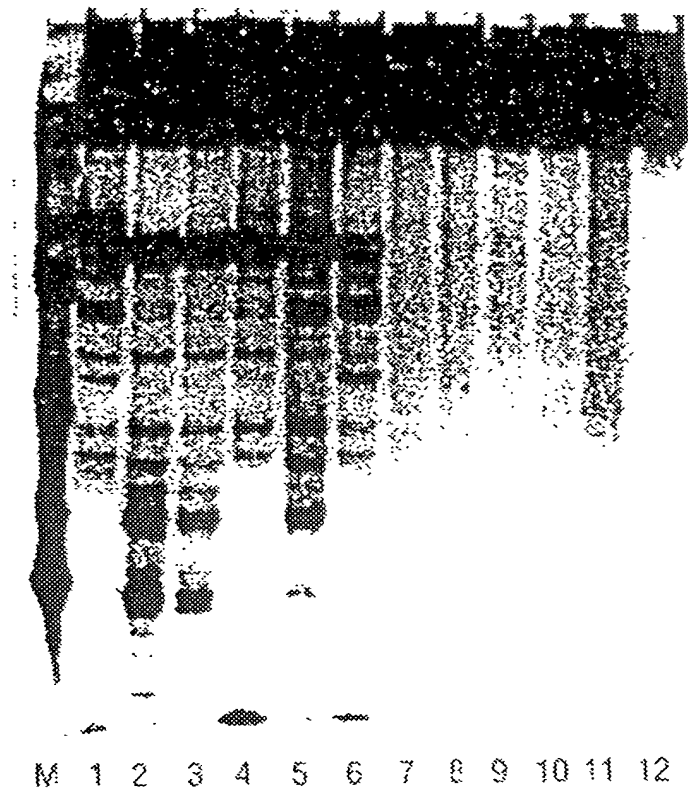


FIG. 50

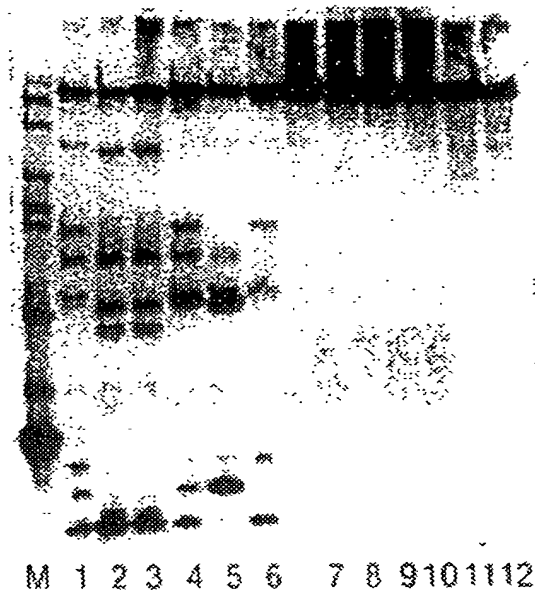


FIG. 51

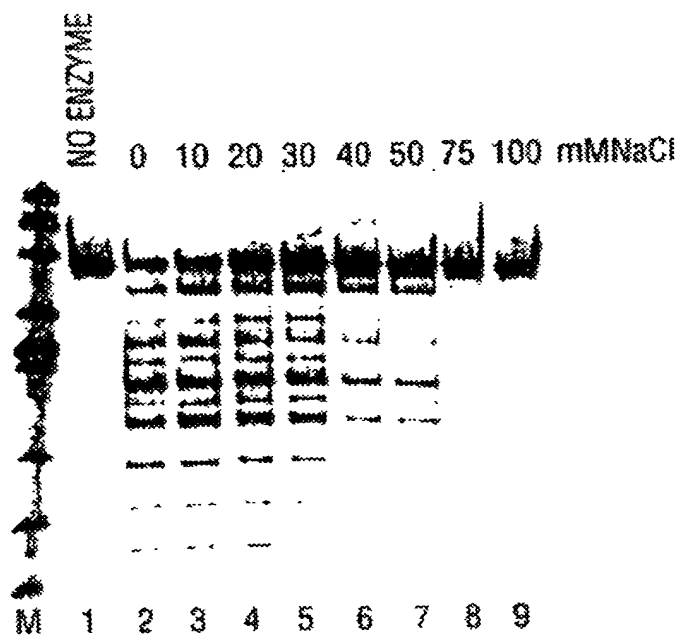


FIG. 52

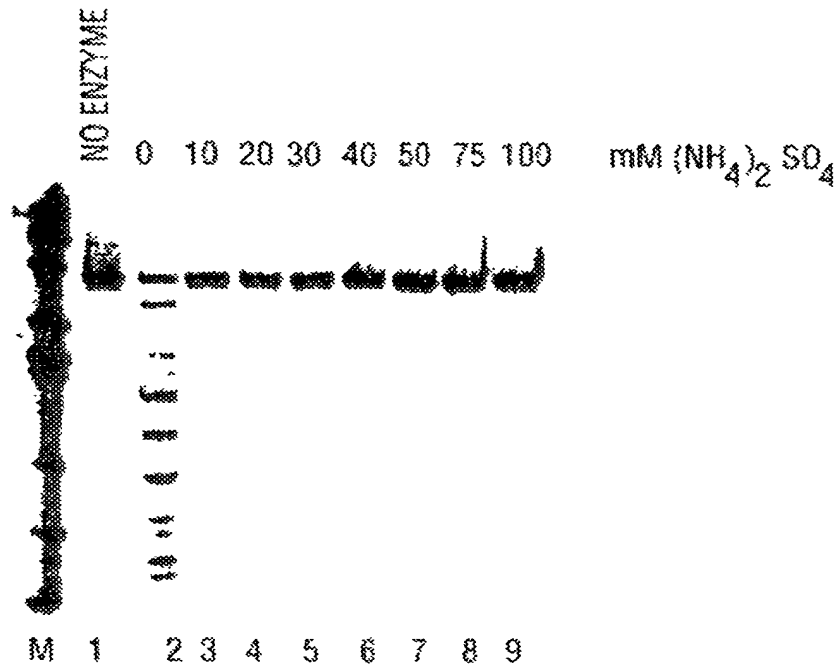


FIG. 53

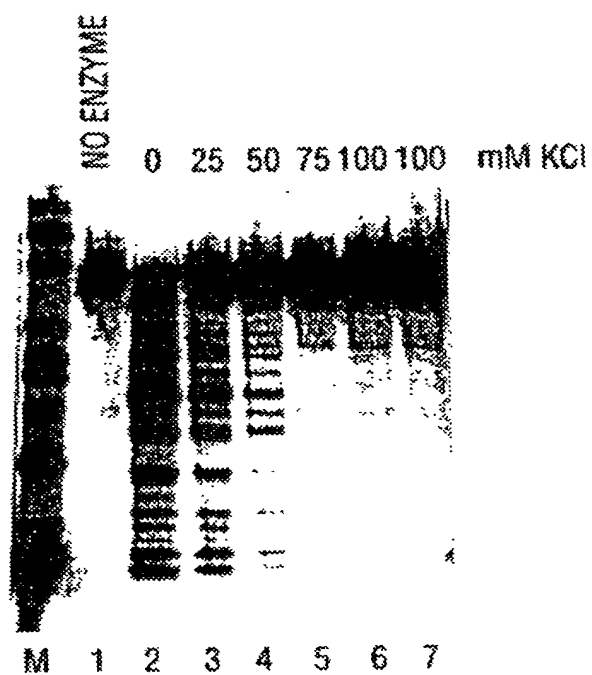


FIG. 54

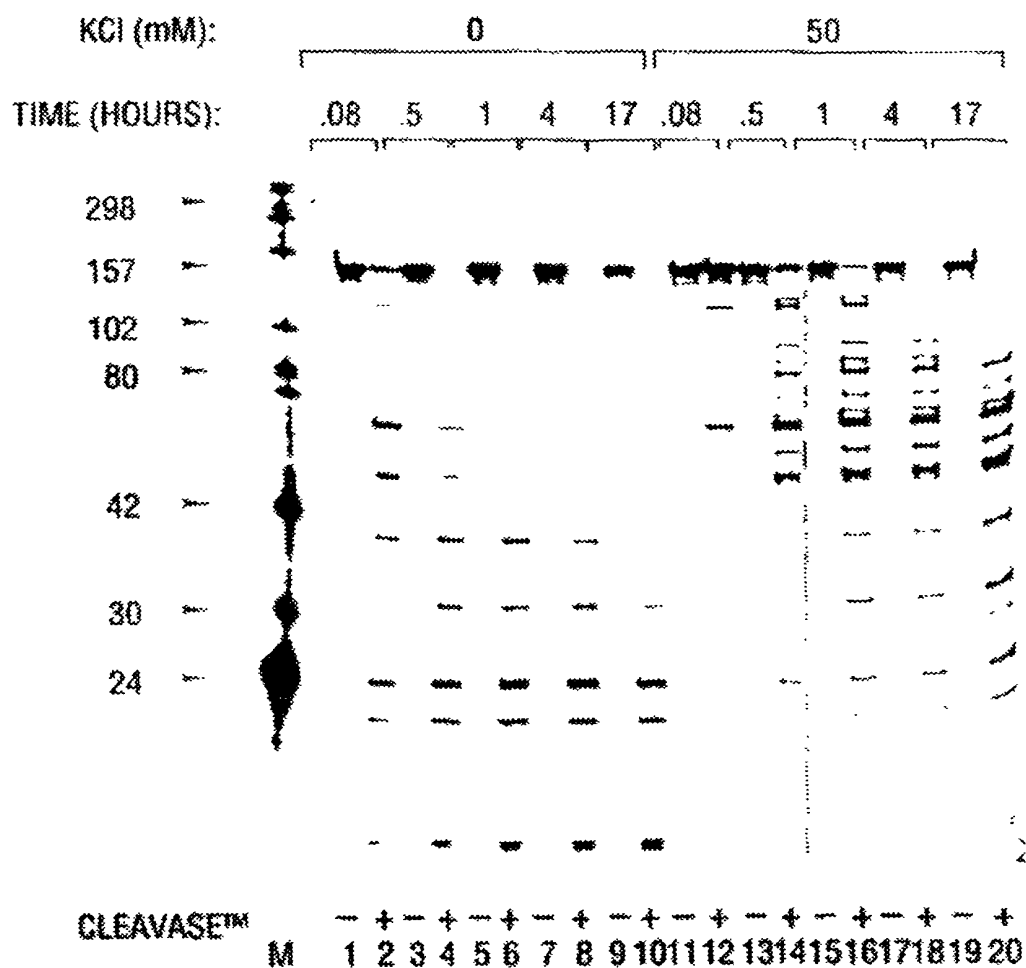


FIG. 55

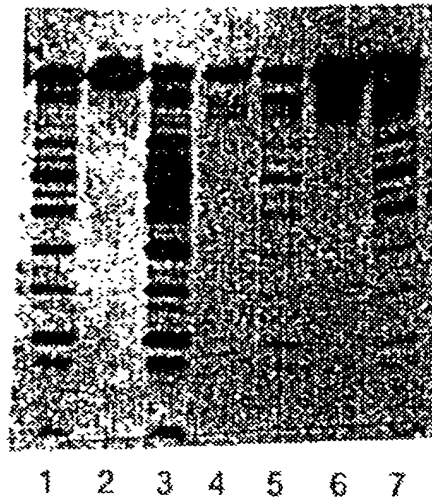


FIG. 56

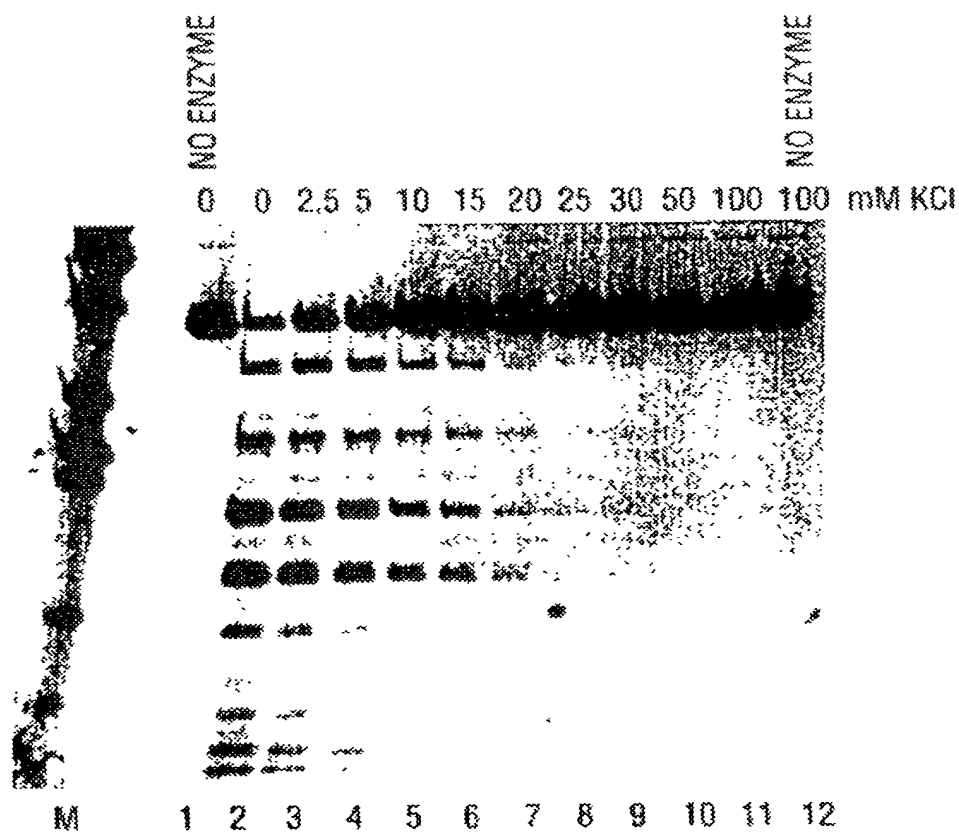


FIG. 57

NO ENZYME

0 0 2.5 5 10 15 20 25 30 50 100 100 mM NaCl

NO ENZYME

M 1 2 3 4 5 6 7 8 9 10 11 12

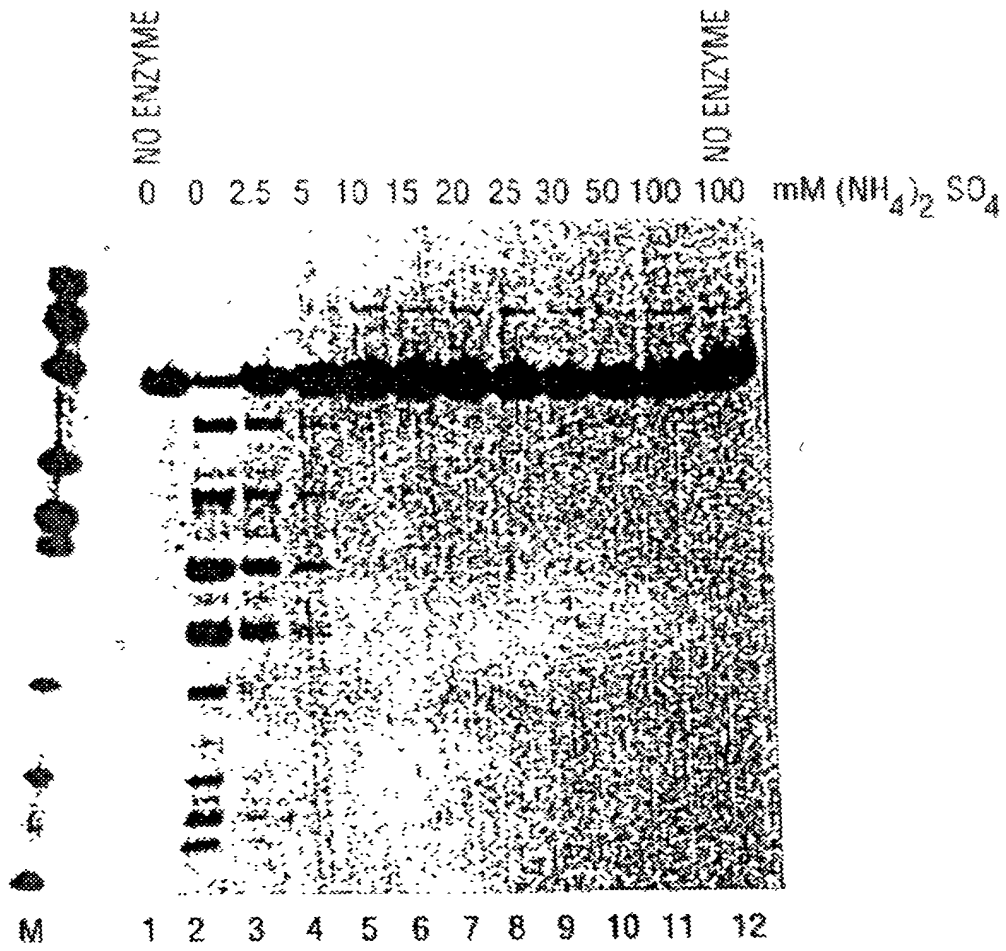


FIG. 59

NO ENZYME

TIME 0 5'' 1' 2' 5 10' 15' 20' 30' 1 HR 2 HR 2 HR NO ENZYME

1 2 3 4 5 6 7 8 9 10 11 12

FIG. 60

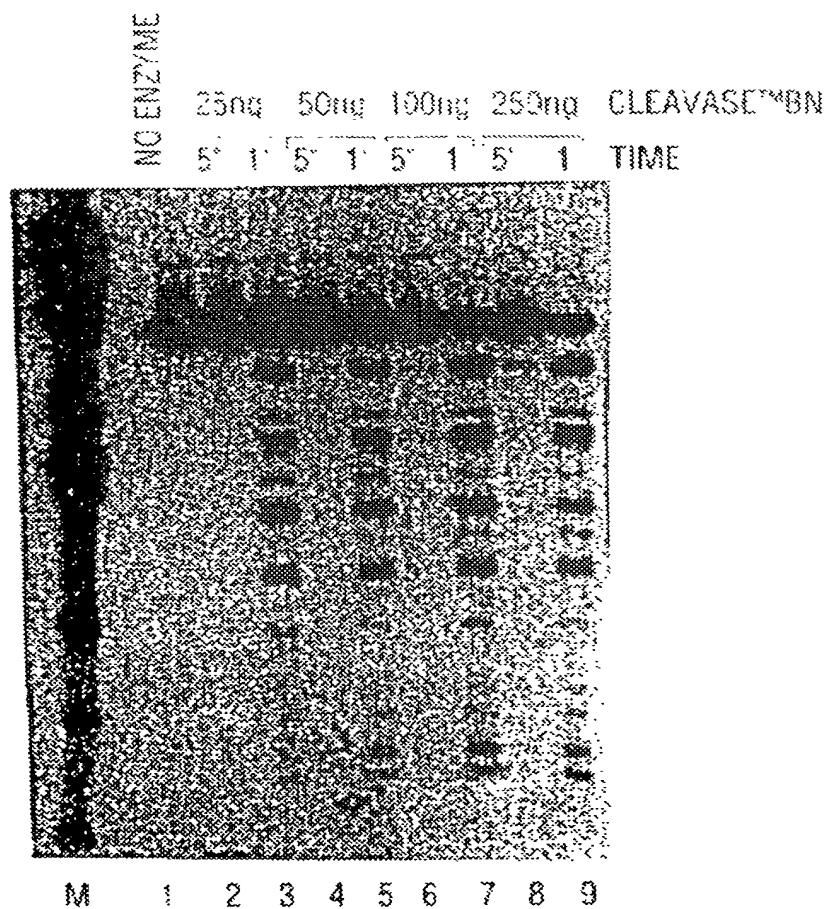


FIG. 61

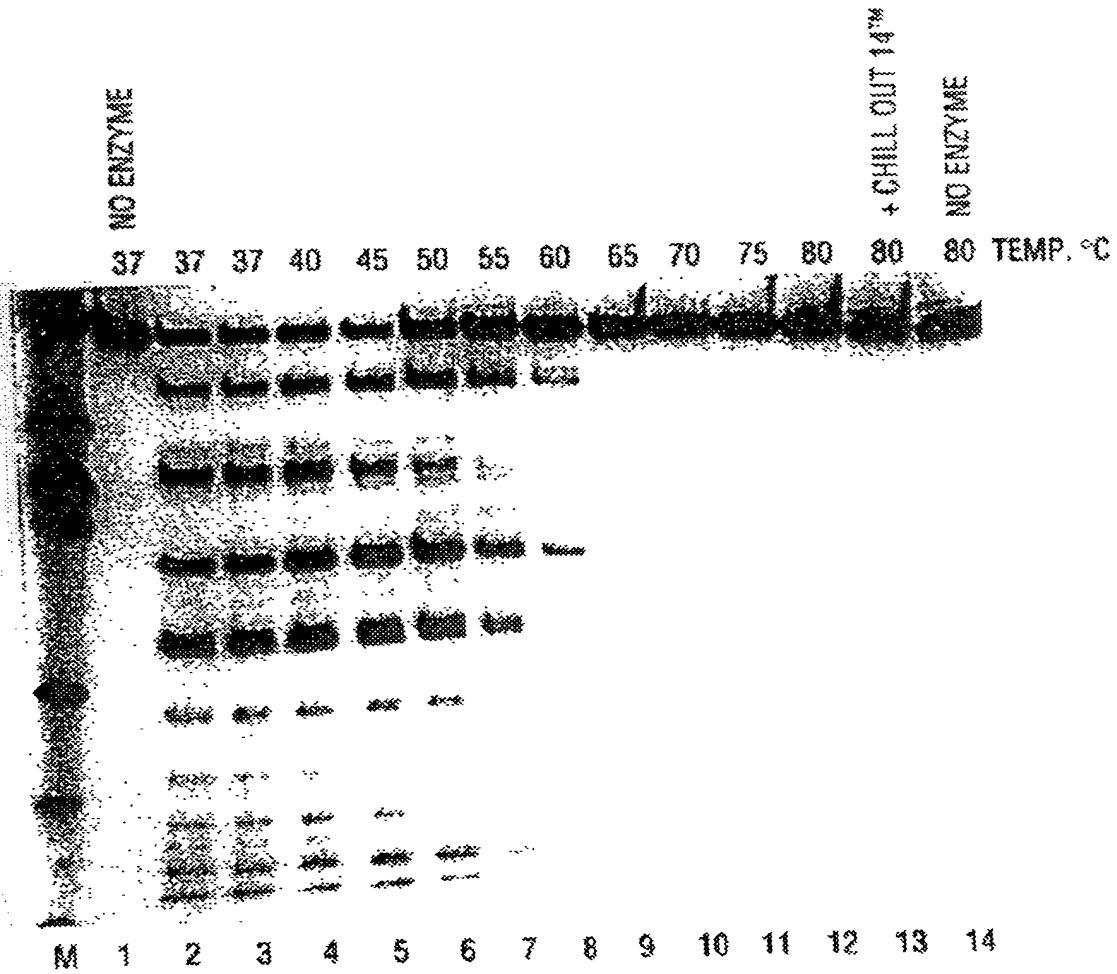


FIG. 62

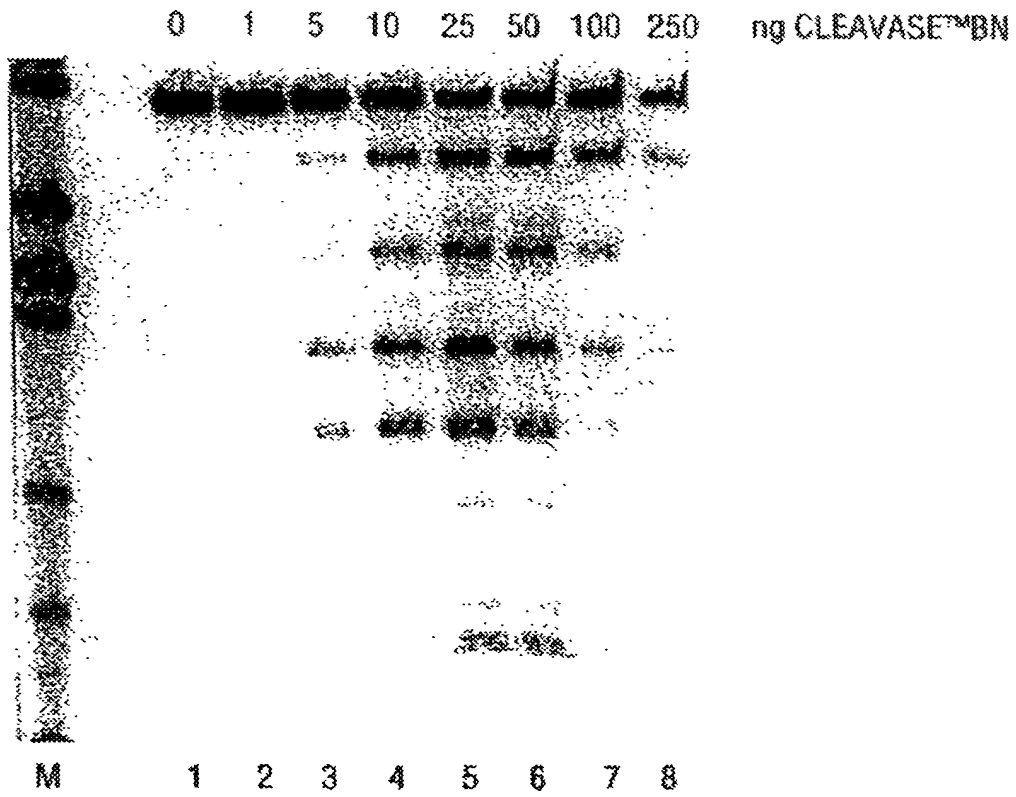


FIG. 63

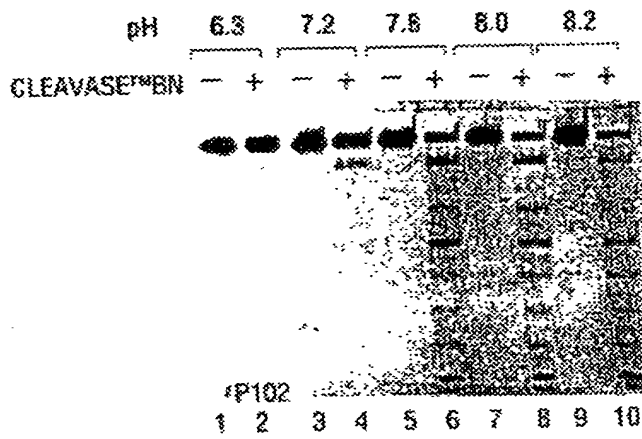


FIG. 64A

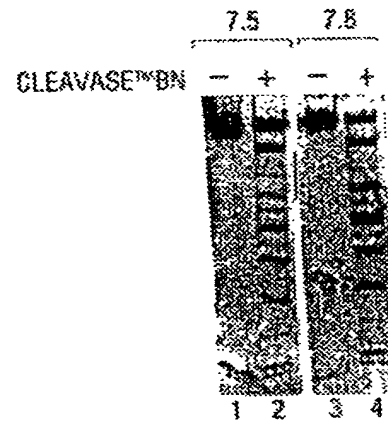
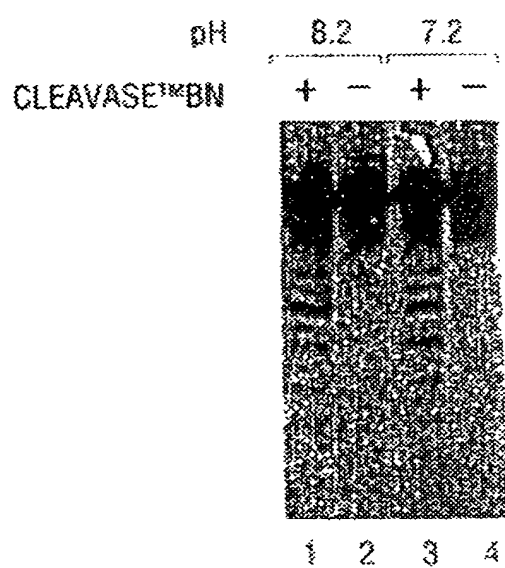


FIG. 64B



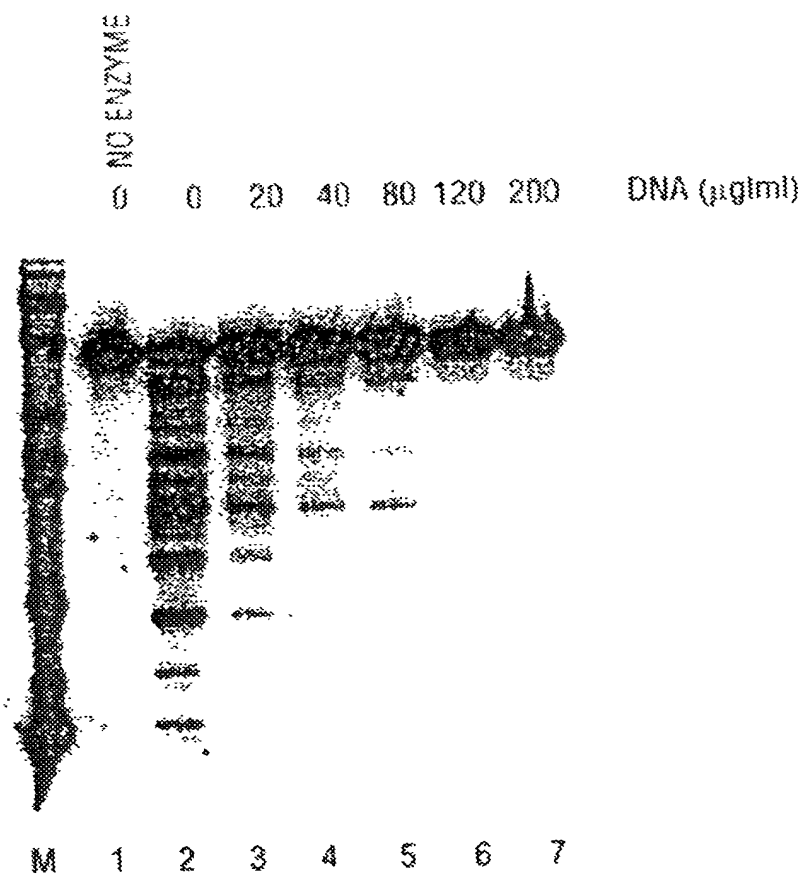


FIG. 66

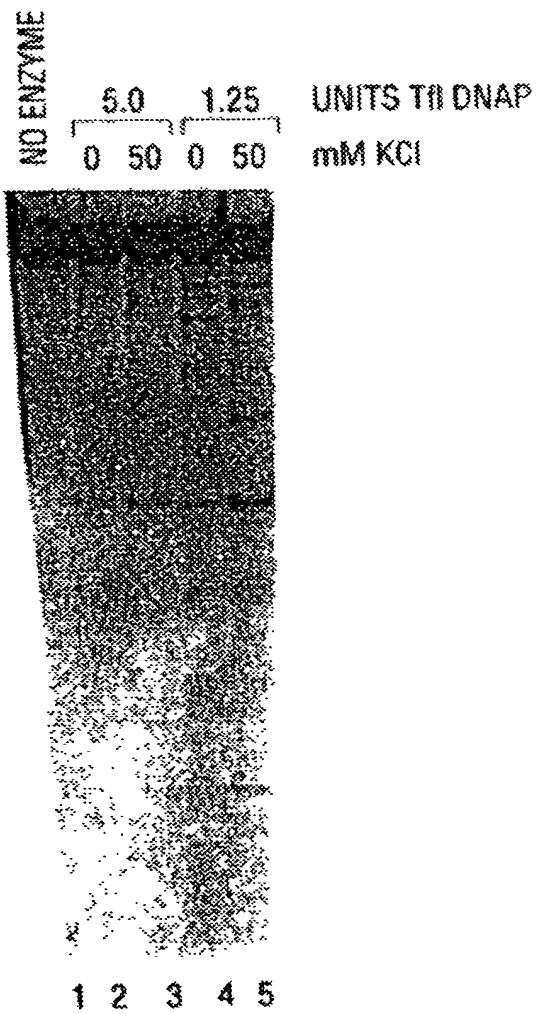


FIG. 67

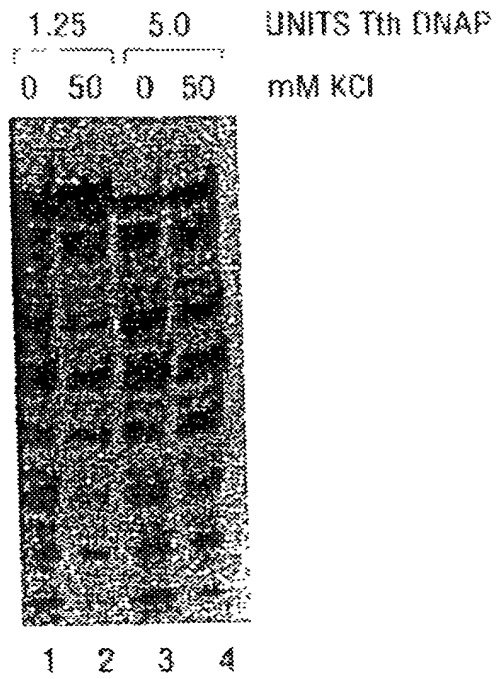


FIG. 68

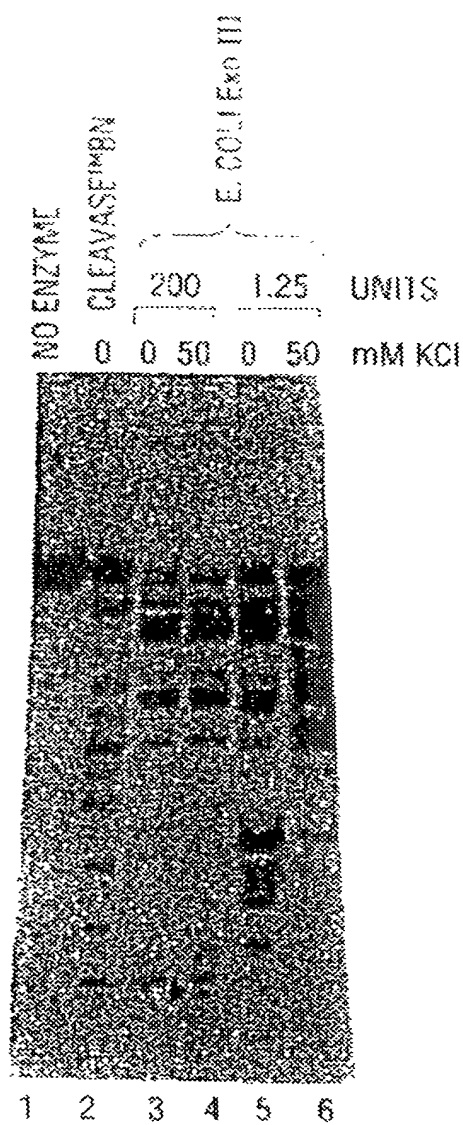


FIG. 69

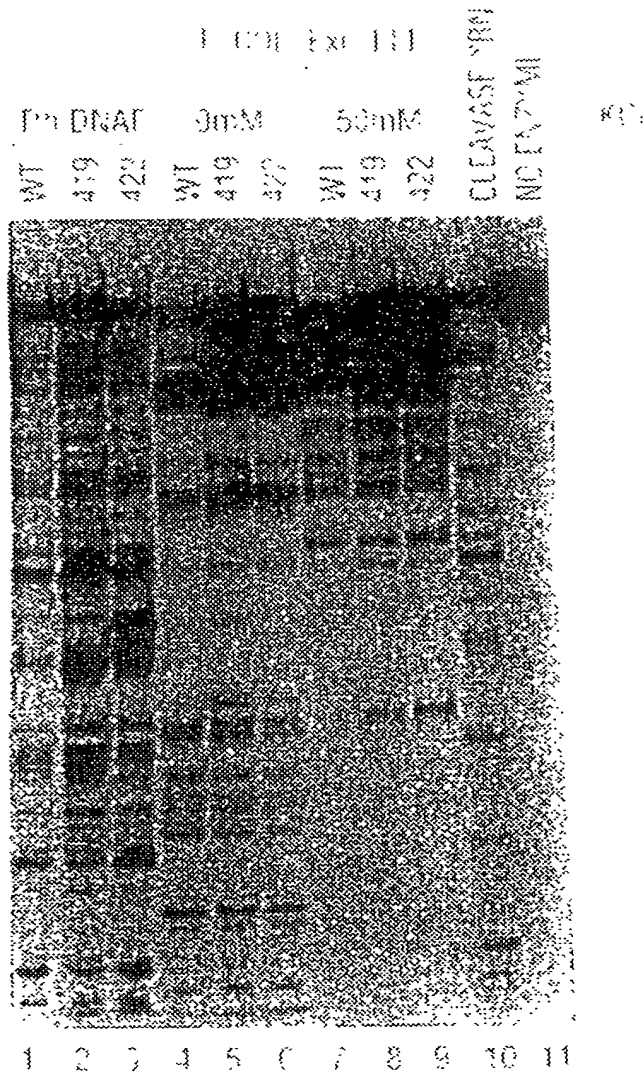
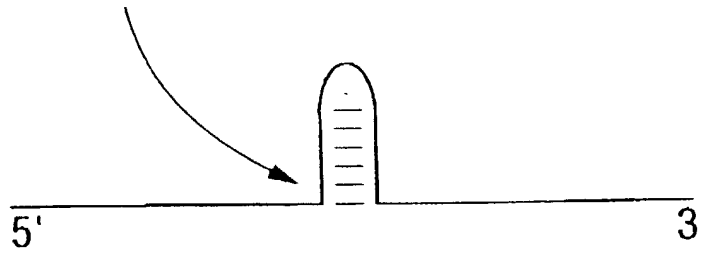


FIG. 70

5' CLEAVAGE SITE



3' CLEAVAGE SITE

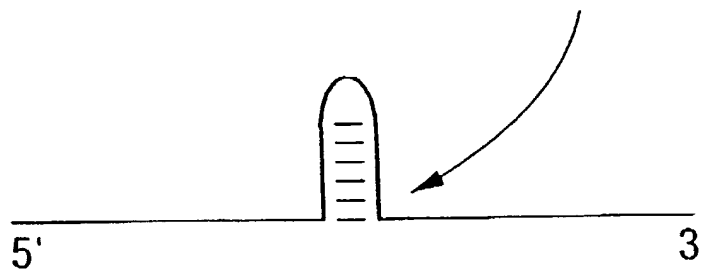


FIG. 71

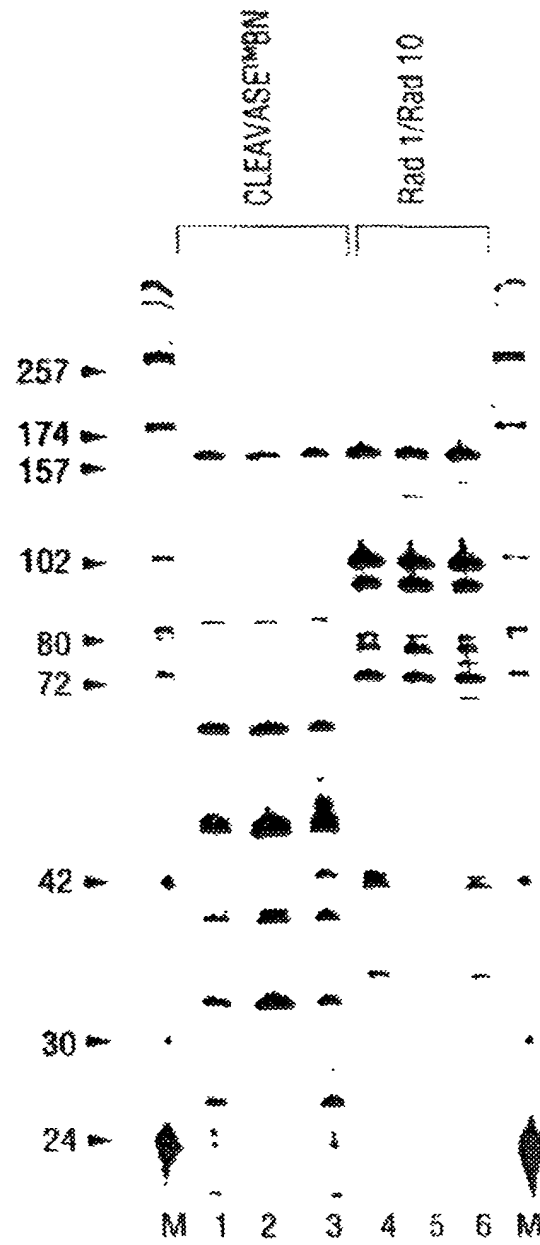


FIG. 72

174



FIG. 73

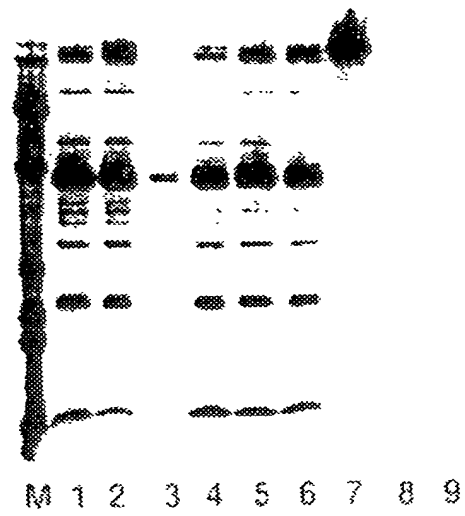


FIG. 75

% OF TOTAL
MUTATIONS

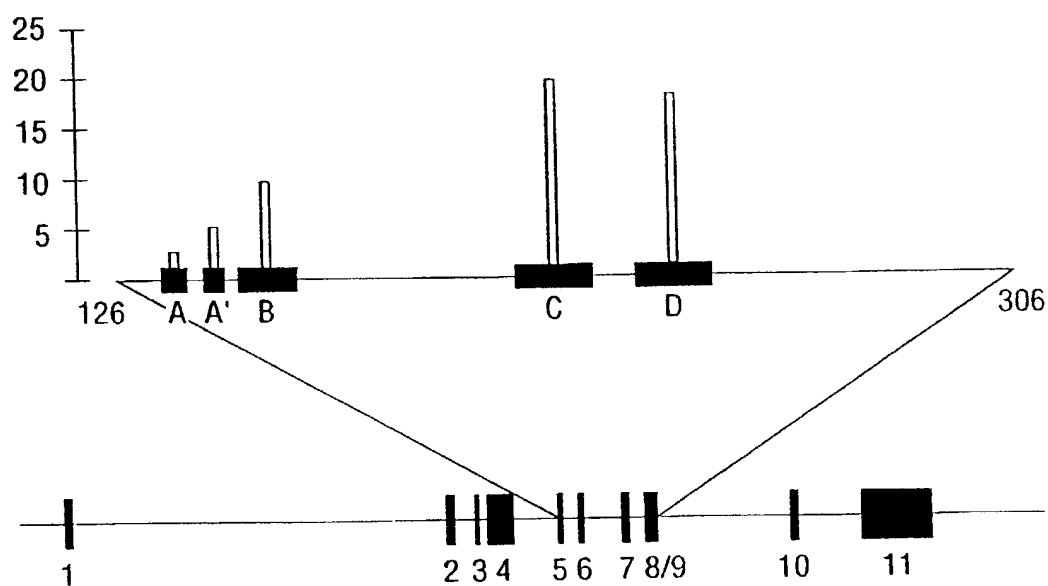


FIG. 76

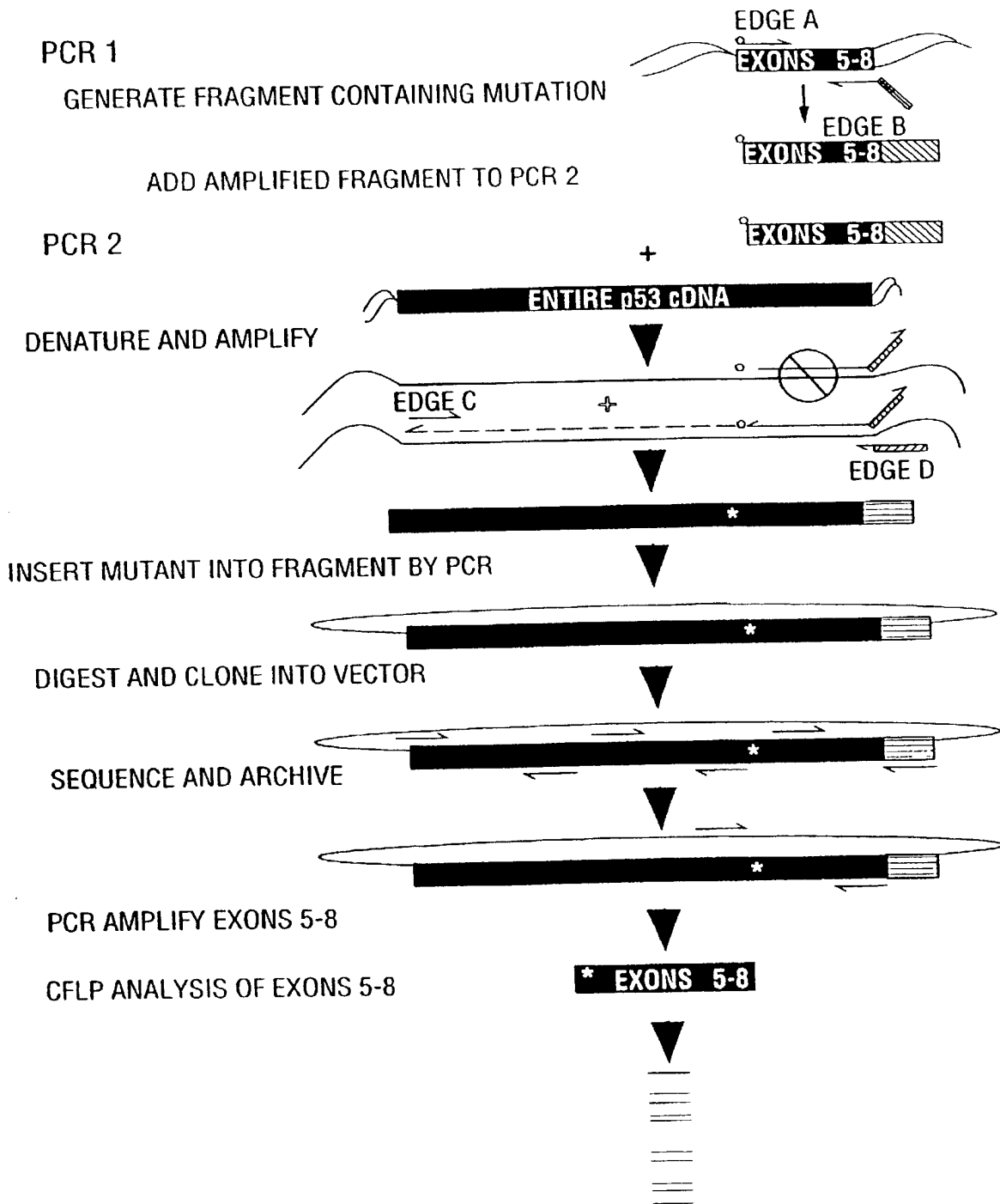


FIG. 77

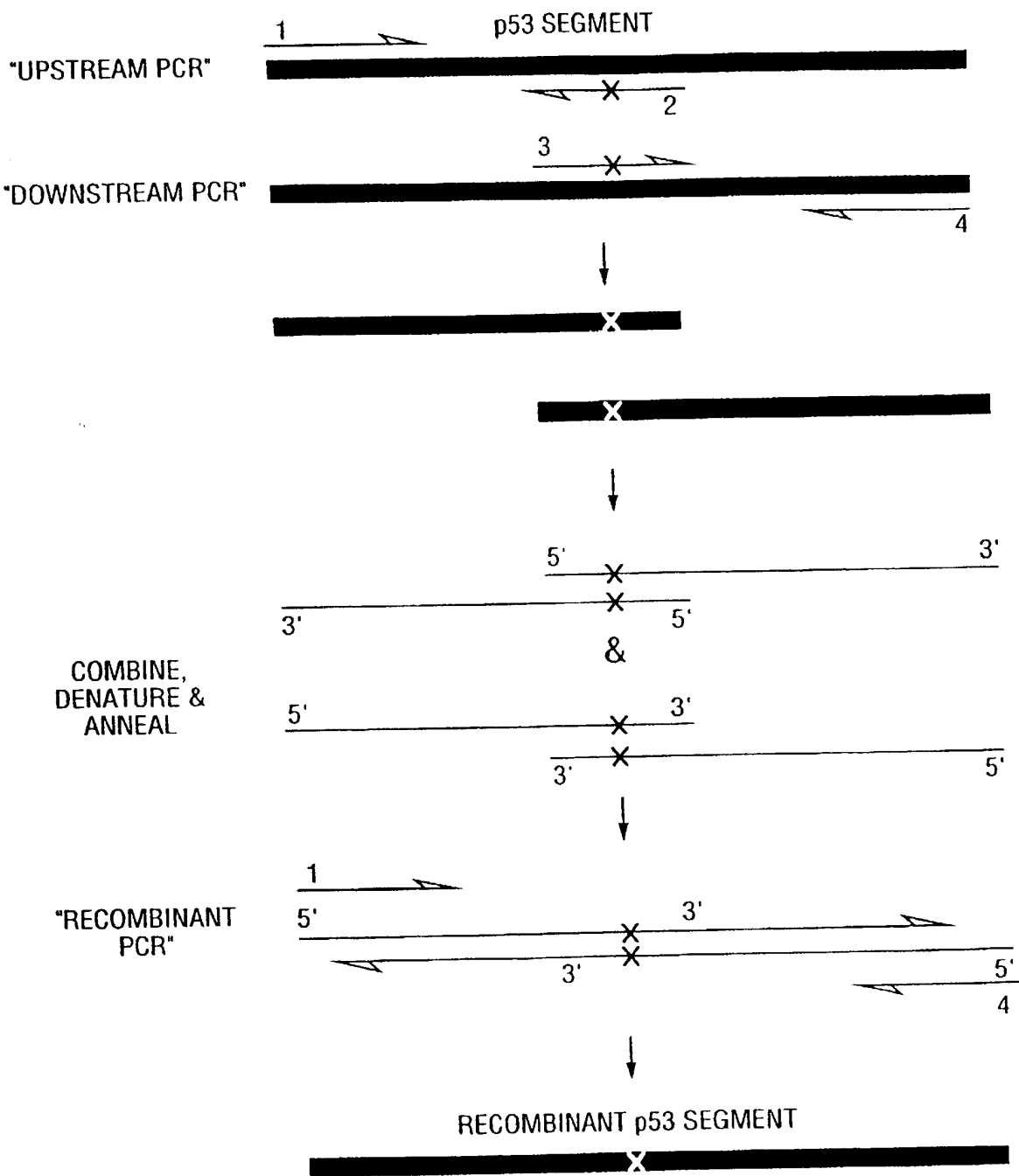


FIG. 78

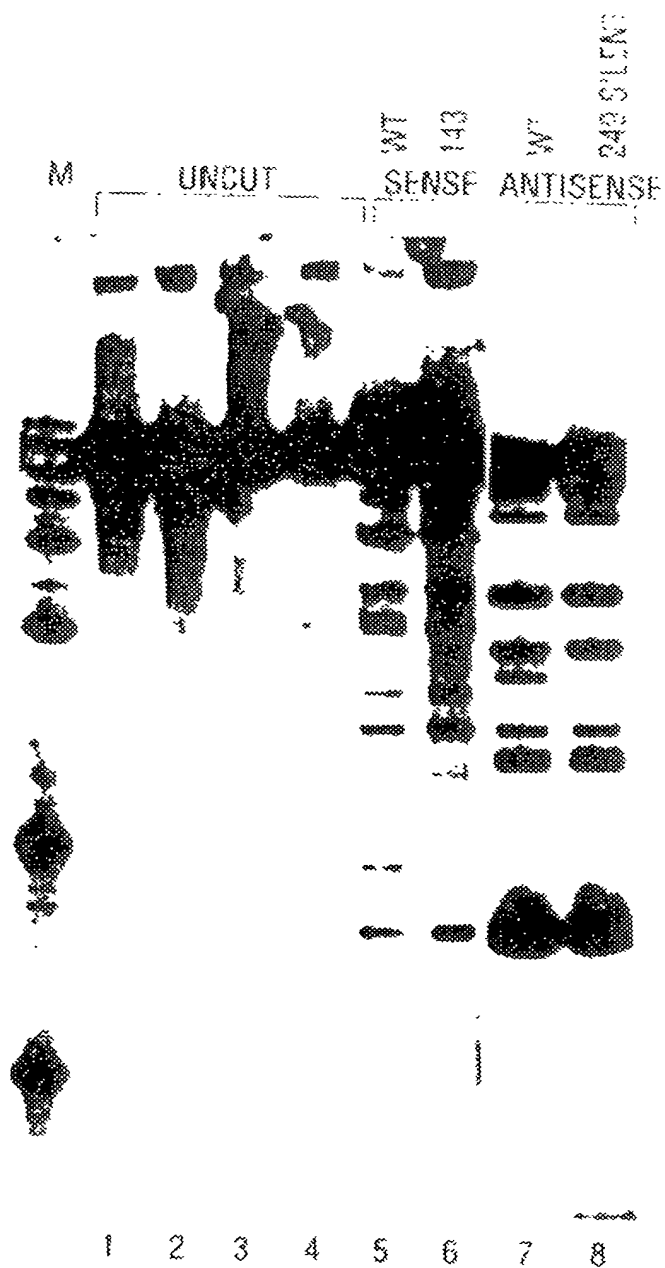


FIG. 79

WT 249 249 273 WT 249 249 273
R +S SILENT R +S SILENT

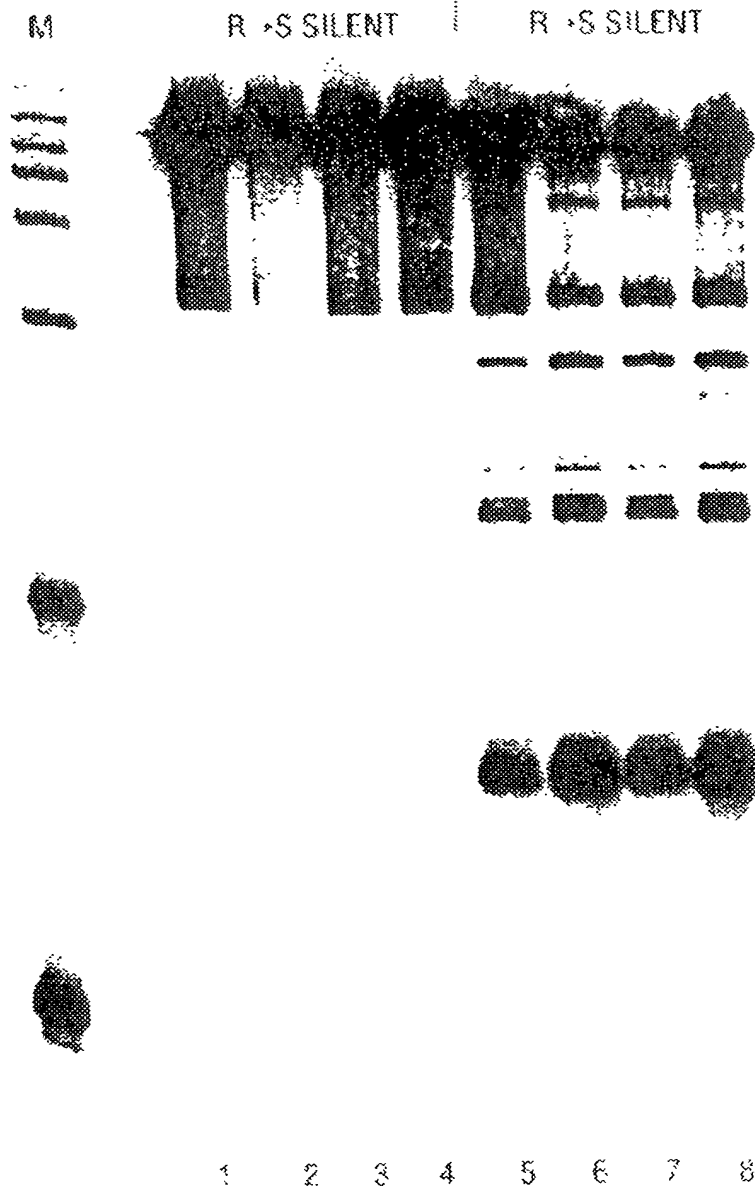


FIG. 80

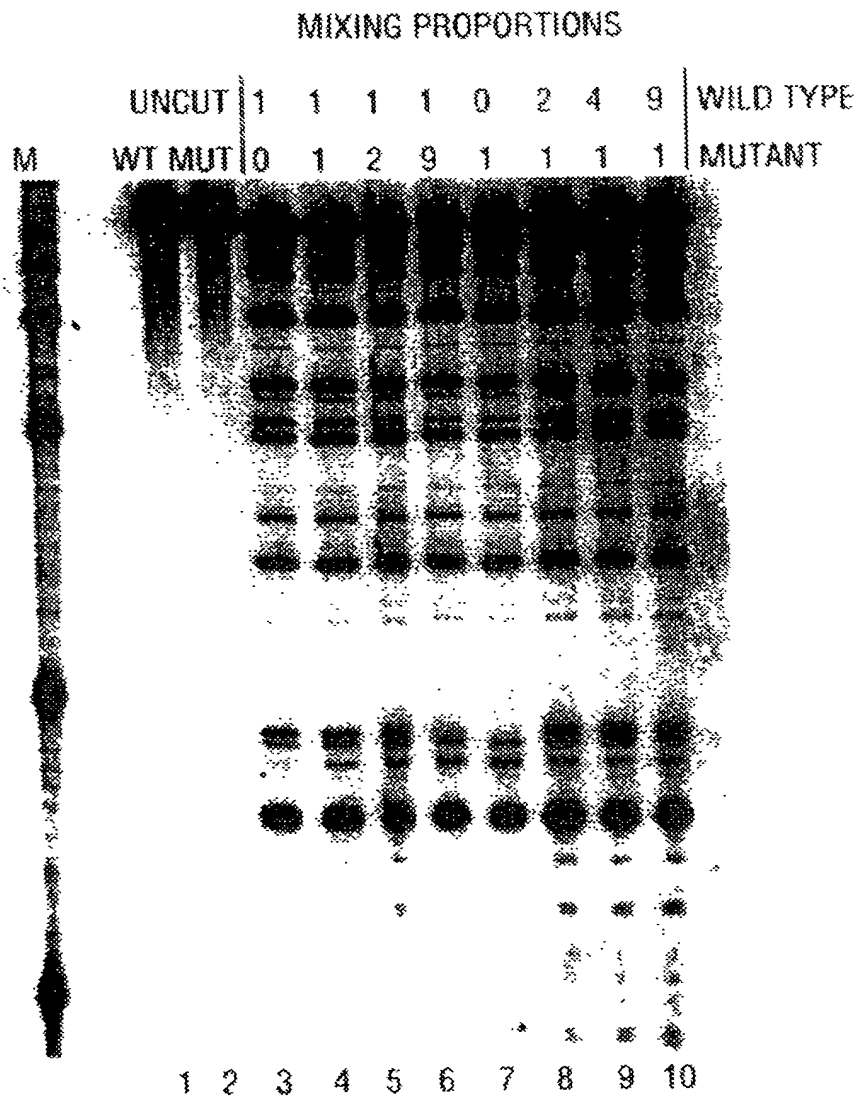


FIG. 81

HCV1.1	151	CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	200
HCV2.1		CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV3.1		CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCGAGA	CTGCTAGCCG	
HCV4.2		CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV6.1		CCCACTCIAT	GCCCGGCCAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV7.1		CCCGCTCAAT	ACCCAGAAAT	TTGGGCGTGC	CCCCGCGAGA	ICACTAGCCG	
HCV1.1	201	AGTAGTGTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCT	250
HCV2.1		AGTAGTGTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV3.1		AGTAGTGTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV4.2		AGTAGTGTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV6.1		AGTAGCGTTG	GGTIGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV7.1		AGTAGTGTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV1.1	251	GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC	282	
HCV2.1		GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV3.1		GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV4.2		GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV6.1		GCGAGTACCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV7.1		GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		

FIG. 82B

CGGAGGTCTCGTAGACCGTGC

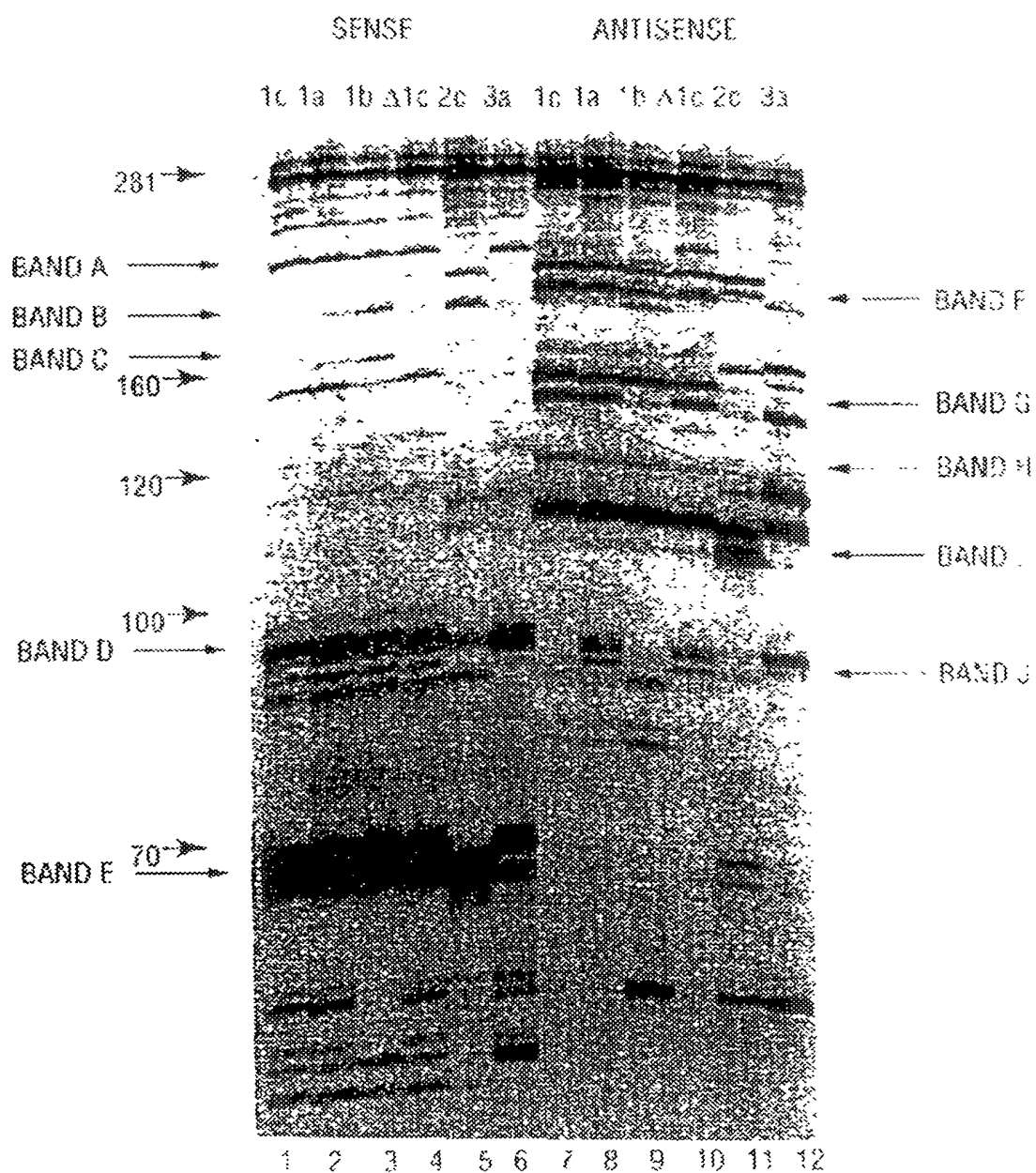


FIG. 83

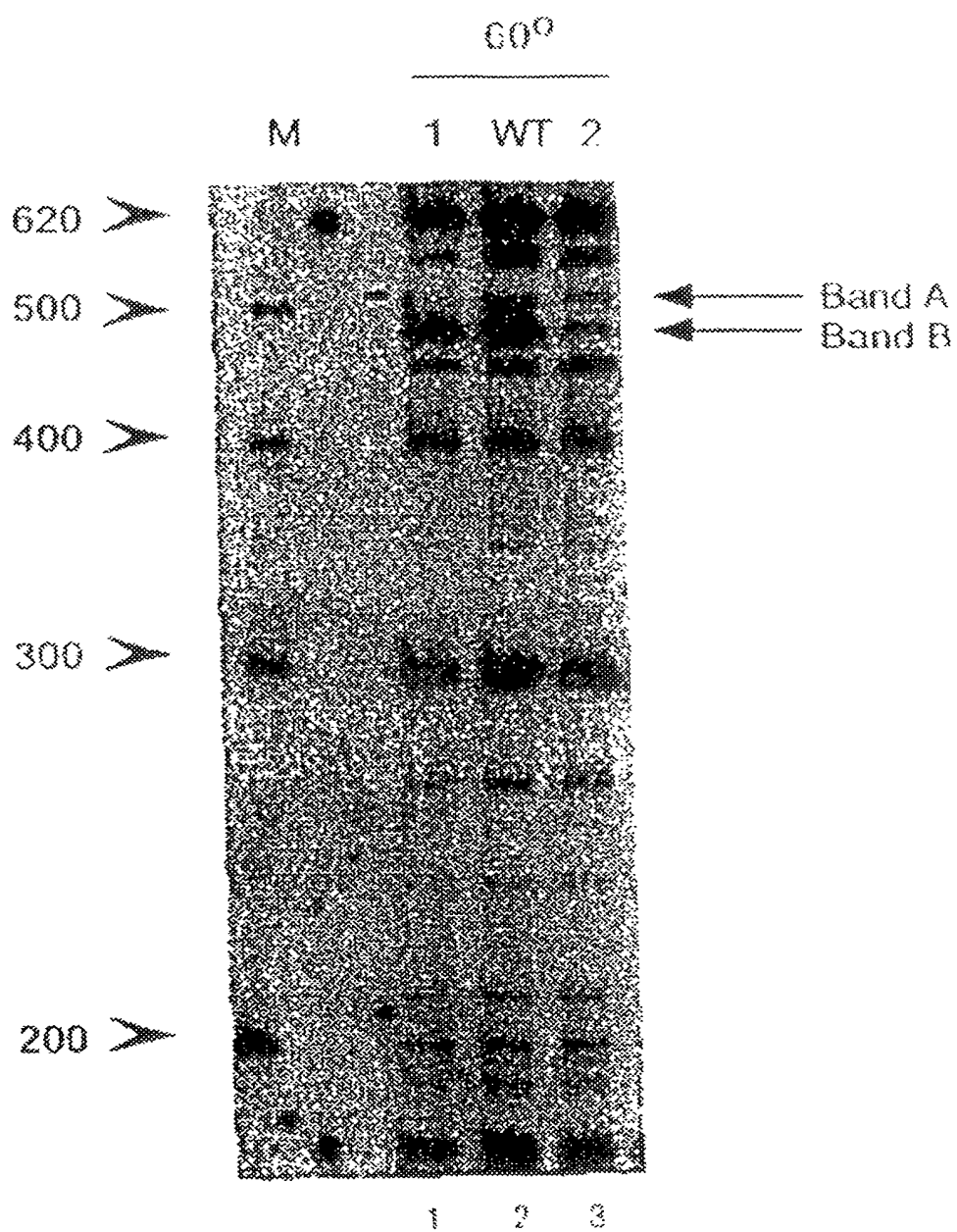


FIG. 84

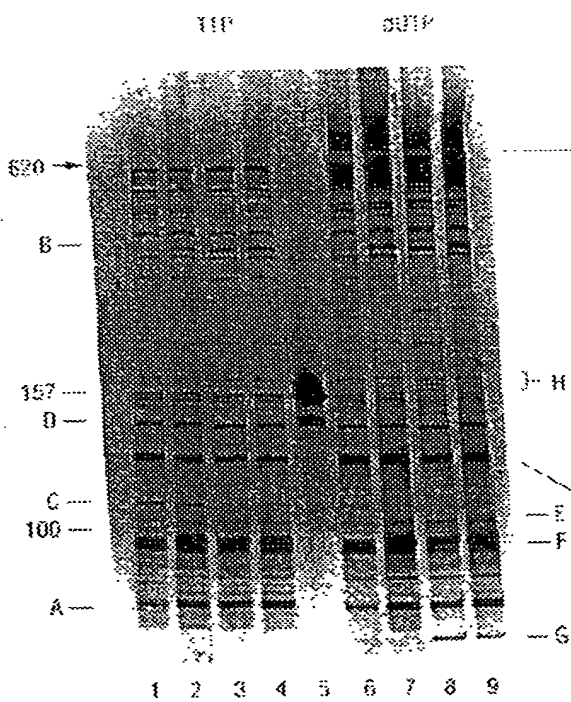


FIG. 85A

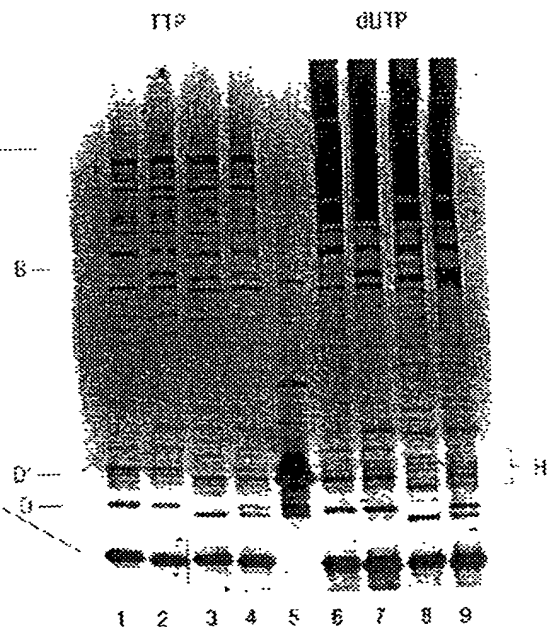


FIG. 85B

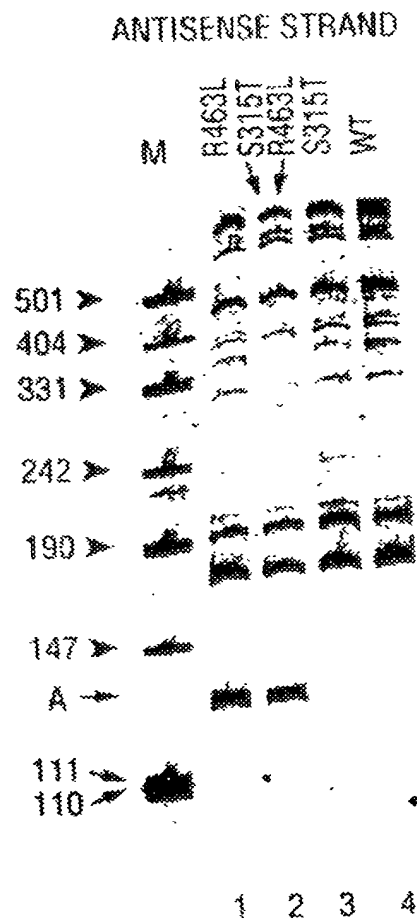


FIG. 87

10	20	30	40	50	60
AGA	GTTTGATCCT	GGCTCAG			
AAATTGAAGA	GTTTGATCAT	<u>GGCTCAGATT</u>	GAACGCTGGC	GGCAGGCCCTA	ACACATGCAA
TTTAACTTCT	CAAACCTAGTA	CCGAGTCTAA	CTTGCGACCG	CCGTCCGGAT	TGTGTACGTT
70	80	90	100	110	120
				GGCGGAC	GGGTGAGTAA
GTCGAACGGT	AACAGGAAGA	AGCTTGCTTC	TTTGCTGACG	<u>AGTGGCGGAC</u>	<u>GGGTGAGTAA</u>
CAGCTTGCCA	TTGTCTTCT	TCGAACGAAG	AAACGACTGC	TCACCGCCTG	CCCACCTCAT
130	140	150	160	170	180
TGTCTGGGAA	ACTGCCTGAT	GGAGGGGGAT	AACTACTGGA	AACGGTAGCT	AATACCGCAT
ACAGACCCCT	TGACGGACTA	CCTCCCCCTA	TTGATGACCT	TTGCCATCGA	TTATGGCGTA
190	200	210	220	230	240
AACGTCGCAA	GACCAAAGAG	GGGGACCTTC	GGGCCTCTTG	CCATCGGATG	TGCCCCAGATG
TTGCAGCGTT	CTGGTTTCTC	CCCCTGGAAG	CCCGGAGAAC	GGTAGCCTAC	ACGGGTCTAC
250	260	270	280	290	300
GGATTAGCTA	GTAGGTGGG	TAACGGCTCA	CCTAGGCGAC	GATCCCTAGC	TGGTCTGAGA
CCTAATCGAT	CATCCACCCC	ATTGCCGAGT	GGATCCGCTG	CTAGGGATCG	ACCAGACTCT
310	320	330	340	350	360
GGATGACCCAG	CCACACTGGA	ACTGAGACAC	GGTCCAGACT	CCTACGGGAG	GCAGCAGTGG
CCTACTGGTC	GGTGTGACCT	TGACTCTGTG	<u>CCAGGTCIGA</u>	<u>GGATGCCCTC</u>	<u>CGTCGICACC</u>
			TGA	GGATGCCCTC	CGTCGTC

FIG. 88A

[illegible]

370	380	390	400	410	420
GGAATATTGC	ACAATGGGCG	CAAGCCCTGAT	GCAGCCCATGC	CGCGTGTATG	AAGAAGGCCT
CCTTATAACG	TGTTACCCGC	GTTCCGACTA	CGTCGGTACG	CGGCACATAC	TTCTTCCGGA
430	440	450	460	470	480
TCGGGTTGTA	AAGTACTTTC	AGCGGGGAGG	AAGGGAGTAA	AGTTAATACC	TTTGCTCATT
AGCCCAACAT	TTCATGAAAG	TCGCCCCCTCC	TTCCTTCATT	TCAATTATGG	AAACGAGTAA
490	500	510	520	530	540
GACGTTACCC	GCAGAAGAAG	CACCGGCTAA	CTCCGTGCCA	GCAGCCGCGG	TAATACGGAG
CTGCAATGGG	CGTCTTCTTC	GTGGCCGATT	GAGGCACGGT	CGTCGGCGCC	ATTATGCCTC
550	560	570	580	590	600
GGTGCAAGCG	TTAATCGGAA	TTACTGGGCG	TAAAGCGCAC	GCAGGCGGTT	TGTTAAGTCA
CCACGTTTCG	AATTAGCCTT	AATGACCCGC	ATTTCCGCTG	CGTCCGCCAA	ACAATTTCAGT
610	620	630	640	650	660
GATGTGAAAT	CCCCGGGCTC	AACCTGGGAA	CTGCATCTGA	TACTGGCAAG	CTTGAGTCTC
CTACACTTTA	GGGGCCCGAG	TTGGACCCTT	GACGTAGACT	ATGACCGTTC	GAACTCAGAG
670	680	690	700	710	720
GTAGAGGGGG	GTAGAAATTCC	AGGTGTAGCG	GTGAAATGCG	TAGAGATCTC	GAGGAATACC
CATCTCCCCC	CATCTTAAGG	TCCACATCGC	CACCTTACGC	ATCTCTAGAC	CTCCTTATGG
730	740	750	760	770	780
GGTGGCGAAG	GCGGCCCCCT	GGACGAAGAC	TGACGCTCAG	GTGCGAAAGC	GTGGGGAGCA
CCACCGCTTC	CGCCGGGGGA	CCTGCTTCTG	ACTGCGAGTC	CACGCTTTTCG	CACCCCTCGT

FIG. 88B

400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780

1210	1220	1230	1240	1250	1260	
ATCATGGCCC	TTA					SB-3
ATCATGGCCC	TTACGA					SB-4
<u>ATCATGGCCC</u>	TTACGACCAG	GGCTACACAC	GTGCTACAAT	GGCGCATACA	AAGAGAAGCG	
TAGTACCGGG	AATGCTGGTC	CCGATGTGTG	CACGATGTTA	CCGCGTATGT	TTCTCTTCGC	
1270	1280	1290	1300	1310	1320	
ACCTCGCGAG	AGCAAGCGGA	CCTCATAAAG	TGCGTCGTAG	TCCGGATTGG	AGTCTGCAAC	
TGGAGCGCTC	TCGTTCCCT	GGAGTATTTC	ACGCAGCATC	AGGCCTAACC	TCAGACGTTG	
1330	1340	1350	1360	1370	1380	
TCGACTCCAT	GAAGTCGGAA	TCGCTAGTAA	TCGTGGATCA	GAATGCCACG	GTGAATACGT	
AGCTGAGGTA	CTTCAGCCTT	AGCGATCATT	AGCACCTAGT	CTTACGGTGC	<u>CACIIAIGCA</u>	1743
				GC	CACIIATGCA	
1390	1400	1410	1420	1430	1440	
TCCCGGGCCT	TGTACACACC	GCCCCGTCACA	CCATGGGAGT	GGGTTGCCAA	AGAAGTAGGT	
<u>AGGGCCCCGA</u>	ACAIGTGTGG	CGGGCAGTGT	GGTACCCTCA	CCCAACGTTT	TCTTCATCCA	
AGGGCCCCGA	ACATG					1743
1450	1460	1470	1480	1490	1500	
AGCTTAACCT	TCGGGAGGGC	GCTTACCCT	TTGTGATTCA	TGACTGGGGT	GAAGTCGTAA	
TCGAATTGGA	AGCCCTCCCC	CGAATGGTGA	AACACTAAGT	ACTGACCCCA	CTTCAGCATT	
1510	1520	1530	1540	1550		
CAAGGTAACC	GTAGGGGAAC	CTGCGGTTGG	ATCACCTCCT	TA.....		
GTTCCATTGG	CATCCCCCTG	GACGCCCAACC	TAGTGGAGGA	AT.....		

FIG. 88D

1638 (SEQ ID NO:151) AGAGTTTGATCCTGGCTCAG
 E.colirrse (SEQ ID NO:158) 0 ...AAATTGAAGAGTTTGATCATGGCTCAGATTGAACGCTGGCGGCAGGCCCTAACACATGCA
 Cam.jejun5 (SEQ ID NO:159) 0 ~TTTTATGGAGAGTTTGATCCCTGGCTCAGAGTGAACGCTGGCGCGTGCCTAATACATGCA
 Stp.aureus (SEQ ID NO:160) 0 ..TTTTATGGAGAGTTTGATCCCTGGCTCAGGATGAACGCTGGCGCGTGCCTAATACATGCA

ER10 (SEQ ID NO:152)
 E.colirrse
 Cam.jejun5
 Stp.aureus

60 AGTCGAACGGTAACAG----GAAGAAGCTTGCTTCTTT----GCTGACGAGTGGCGGACGGG
 62 AGTCGAACGAT-----GAAGCTTCTAGCTTGCTAGAAGTGA-----TTAGTGGCGCACGGG
 61 AGTCGAGCGAA-----CGGACGAGAAGCTTGCTTCTCTGATG----TT-AGCGGCGGACGGG
 GCGGACGGG

ER10
 E.colirrse
 Cam.jejun5
 Stp.aureus

114 TGAGTAATGTCTGGGA-AACTGCCTGATGGAGGGGATAACTACTGGAACGGTAGCTAATA
 114 TGAGTAAGGTATAGTTAATCTGCCCTACACAAGAGGACAACAGTTGGAAACGACTGCTAATA
 113 TGAGTAACACGCTGGATAACCTACCTAAGACTGGGATAACTTCGGGAACCGGAGCTAATA

E.colirrse
 Cam.jejun5
 Stp.aureus

175 CCGCATAAC-----GTCGCAAGAC-----CAAAGAGGGGACCTTCG-GGCCTCTTG
 176 CTCTATACTCCTGCTTAACACAAGTTGAGTAGG-GAAAG-----TTTTT-----CG
 175 CCGGATAATATTTTGAACCGCATGGTTCAAAAGTGAAAGACGGT----CTT----GCTGTCA

E.colirrse
 Cam.jejun5
 Stp.aureus

221 CCATCGGATGTGCCCAGATGGGATTAGCTAGTGGGTAAACGGCTCACCTAGGCGACGA
 221 GTGTAGGATGAGACTATATAGTATCAGCTAGTTGGTAAGGTAATGGCTTACCAAGGCTATGA
 229 CTTATAGATGGATCCGCGCTGCATTAGCTAGTTGGTAAGGTAAACGGCTTACCAAGGCAACGA

E.colirrse
 Cam.jejun5
 Stp.aureus

283 TCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACGTGAGACACGGTCCAGACTCCCTA
 283 CGCTTAACCTGGTCTGAGAGGATGATCAGTCACACTGGAACGTGAGACACGGTCCAGACTCCCTA
 291 TACGTAGCCGACCTGAGAGGGTGATCGGCCACACTGGAACGTGAGACACGGTCCAGACTCCCTA
 1659 (COMPL) ACTCCTA

FIG. 89A

FIG. 89A

E.colirrsE
Cam.jejun5
Stp.aureus
1659 (COMPL)

345 CGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCGCGTG
345 CGGGAGGCAGCAGTAGGGAATATTGCGCAATGGGGAAACCCCTGACGCAGCAACGCCGCGTG
353 CGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGCCTGACGGAGCAACGCCGCGTG
CGGGAGGCAGCAG

E.colirrsE
Cam.jejun5
Stp.aureus

407 TATGAAGAAGGCCTTCGGGTTGTAAAGTACTTTCAGCGGGGAGGAA-GGGAGTAAAGTTAAT
407 GAGGATGACACTTTTCGGAGCGTAAACTCCTTTTCTTAGGGAAG -----AATT
415 AGTGATGAAGGTCTTCGGATCGTAAACTCTGTTATTAGGGAAGAACATATGTGTAAGTAAC

E.colirrsE
Cam.jejun5
Stp.aureus

468 ACCTTTGCTCATTGACGTTACCCGCAGAAGAAGCACCCGGCTAACTCCGTGCCAGCAGCCGCG
455 C-----TGACGGTACCTAAGGAATAAGCACCGGCTAACTCCGTGCCAGCAGCCGCG
476 -TGTGCACATCTTGACGGTACCTAATCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCG

FIG. 89B

FIG. 89B

E.colirrsE	530	GTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGCGTAAAGCGCACGCAGGCGGTTT
Cam.jejun5	506	GTAATACGGAGGGTGCAAGCGTTAATCGGAATCACTGGCGTAAAGGCGCGTAGGCGGATT
Stp.aureus	538	GTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGCGCGTAGGCGGTTT
E.colirrsE	592	GTTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATCTGATACTGGCAAGCTT
Cam.jejun5	568	ATCAAGTCTCTTGTGAAATCTAATGGCTTAACCATTAACCTGCTTGGGAACTGATAGTCTA
Stp.aureus	600	TTTAAGTCTGATGTGAAAGCCACGGCTCAACCGTGGAGGTCATTGGAACTGGAAACTT
E.colirrsE	654	GAGTCTCGTAGAGGGGGGTAGAAATCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGA
Cam.jejun5	630	GAGTGAGGGAGAGGCAGATGGAAATTGGTGGTGTAGGGGTAAATCCGTAGATATCACCAAGA
Stp.aureus	662	GAGTGCAGAAAGAGGAAGTGGAATTCATGTGTAGCGGTGAAATGCGCAGAGATATGGAGGA
E.colirrsE	716	ATACCGGTGGCGAAGGCGGCCCCCTGGACGAAGACTGACGCTCAGGTGCCGAAAGCGTGGGGA
Cam.jejun5	692	ATACCCATTGCGAAGGCGATCTGCTGGAACTCAACTGACGCTAAGGCGCGAAAGCGTGGGGA
Stp.aureus	724	ACACCACTGGCGAAGGCGACTTCTGTGCTGTAACTGACGCTGATGTGCCGAAAGCGTGGGGA
E.colirrsE	778	GCAAACAGGATTAGATACCCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGTGC
Cam.jejun5	754	GCAAACAGGATTAGATACCCCTGGTAGTCCACGCCCTAAACGATGTACACTAGTTGTTGGGGT
Stp.aureus	786	TCAAACAGGATTAGATACCCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGG

FIG. 89C

<i>E.colirrsE</i>	840	C-CTTGA-GGCGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCCGC
<i>Cam.jejun5</i>	816	G-CTAGT-CATCTCAGTAATGCAGCTAACGCCATTAAAGTGTACCGCCTGGGGAGTACGGTCGC
<i>Stp.aureus</i>	848	GT-TTCCGCCCCCTTAGTGCTGCAGCTAACGCATTAAAGCACTCCGCCTGGGGAGTACGACCCG
<i>E.colirrsE</i>	900	AAGGTTAAACTCAAATGAATTGACGGGGGCCCGCACAAAGCGGTGGAGCATGTGTTTAATT
<i>Cam.jejun5</i>	876	AAGATTAAACTCAAAGGAATAGACGGGGACCCGCCACAAGCGGTGGAGCATGTGTTTAATT
<i>Stp.aureus</i>	909	AAGGTTGAACTCAAAGGAATTGACGGGGACCCGCCACAAGCGGTGGAGCATGTGTTTAATT
<i>E.colirrsE</i>	962	CGATGCAACGCCGAAGAACCTTACCTGGTCTTGACATCCACGGAAGTTTTTCAGAGATGAGAAT
<i>Cam.jejun5</i>	938	CGAAGATACGCCGAAGAACCTTACCTGGGCTTGATATCCTAAGAACCTTTTTCAGAGATAAGAGG
<i>Stp.aureus</i>	971	CGAAGCAACGCCGAAGAACCTTACCAAATCTTGACATCCTTTTGACAACTCTAGAGATAGAGCC
<i>E.colirrsE</i>	1024	GTG--CCTTCGGG--AA-CCGTGAGACAGGTGCTGCATGGCTGTCGTACGCTCGTGTGTGA
<i>Cam.jejun5</i>	1000	GTGCTAGCTTGCTAGAA-CTTAGAGACAGGTGCTGCACGGCTGTCGTACGCTCGTGTGTGA
<i>Stp.aureus</i>	1033	TTCC-CCTTCGGG--GGACAAAGTGACAGGTGGTGCATGGTTGTCGTACGCTCGTGTGTGA
SB-1		GCAACGAGCGCAACCC
<i>E.colirrsE</i>	1081	AATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGGTCCGG-CC
<i>Cam.jejun5</i>	1061	GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCACGTAATTTAGTTGCTAACGGTTCGG-CC
<i>Stp.aureus</i>	1092	GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTAAGCTTAGTTGCCATCA-TTAAGT-T

FIG. 89D

SB-3 (SEQ ID NO:157)	ATGACGTC	CAAGTCATC
SB-4 (SEQ ID NO:154)	ATGACGTC	CAAGTCATC
E.colirrsE	1142	GGGAAC
Cam.jejun5	1122	GAGCACTCTAAATAGACTGCCTTCG-TAAGGAGGAGGAAGGTGTGGACGACGTCAAGTCATC
Stp.aureus	1152	GGGCACTCTAAGTTGACTGCCGGTGACAAACCGGAGGAAGGTGGGATGACGTCAAATCATC
SB-3		ATGGCCCCCTTA
SB-4		ATGGCCCCCTTACGA
E.colirrsE	1204	ATGGCCCCCTTACGACACGGGTACACACGTGCTACAAATGGCGCATACAAAAGAGAGCGACCTC
Cam.jejun5	1183	ATGGCCCCCTTATGCCACGGCGACACACGTGCTACAAATGGCATATAGAAATGAGACGCAATACC
Stp.aureus	1214	ATGGCCCCCTTATGATTTGGGCTACACACGTGCTACAAATGGACAATACAAAGGGCAGCGAAACC
E.colirrsE	1266	GCGAGAGCAAGCGGACCTCATAAAGTGCGTTCGTAGTCCGGATTGGAGTCTGCAACTCGACTC
Cam.jejun5	1245	GCGAGGTGGAG-CAAACTCTATAAAATATGTCCAGTTCGGATTGTTCTCTGCAACTCGAGAG
Stp.aureus	1276	GCGAGGTCAAGCAAATCCCATAAAGTTGTTCTCAGTTCGGATTGTAGTCTGCAACTCGACTA
E.colirrsE	1328	CATGAAGTCGGAATCGCTAGTAATCGTGGATCAGA-ATGCCACGGTGAATACGTTCCCGGGC
Cam.jejun5	1306	CATGAAGCCGGAATCGCTAGTAATCGTAGATCAGCCATGCTACGGTGAATACGTTCCCGGGT
Stp.aureus	1338	CATGAAGCTGGAATCGCTAGTAATCGTAGATCAGC-ATGCTACGGTGAATACGTTCCCGGGT
1743 (compl)		CGGTGAATACGTTCCCGGGC

FIG. 89E

E.colirrsE	1389	CTTG	TACACACCGCCCGT	CACACCATGGGAGTGGGTTG	CAAAAGAGTAGG	TAGCTTAACCT
Cam.jejun5	1368	CTTG	TACTACCGCCCGT	CACACCATGGGAGTTG	ATTTCACTCGAAGCCGGA	TACT--A-A
Stp.aureus	1399	ATTG	TACACACCGCCCGT	CACACACGAGAGTTT	GTAAACACCCGAAGCCGGT	GGAGTAACCT
1743(compl)		CTTG	TAC			
E.colirrsE	1451	TCG	GGAGGGCGCTT	ACCACCTTTGTGATT	CATGACTGGG	TGAAGTCGTAACAAGGTAACCG
Cam.jejun5	1427	AC--	T-AGTTACCGTCCACAGT	GGAATCAGCGACTGGGGT	GAAAGTCGTAACAAGGTAACCG	
Stp.aureus	1461	TTTAGGAGCTAGCCGTCGAAGGTGGGACAAATGATTGGGGTGAAGTCGTAACAAGGTAAGCCG				
E.colirrsE	1512	TAGGGGAACCTGCGGTTGGATCACCTCCTTA---				
Cam.jejun5	1485	TAGGAGAACCTGCGGTTGGATCACCTCCT-----				
Stp.aureus	1523	TATCGGAAGGTGCGGCTGGATCACCTCCTTTCT-				

FIG. 89F

[REDACTED]

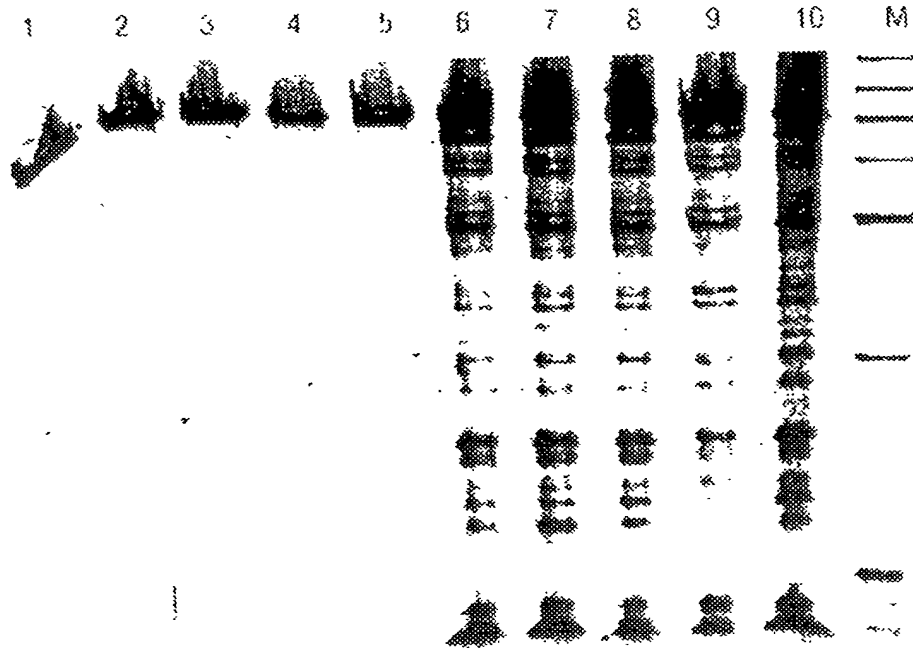


FIG. 91A

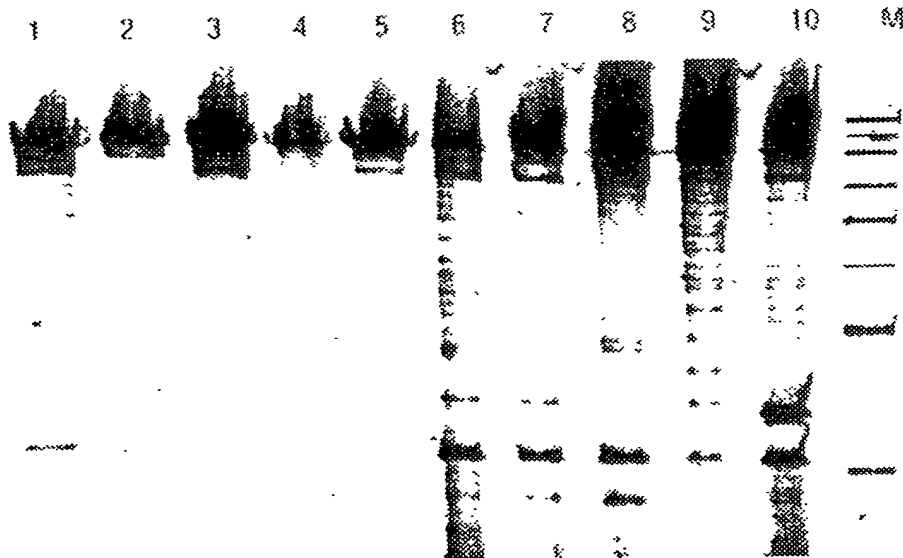


FIG. 91B



FIG. 92

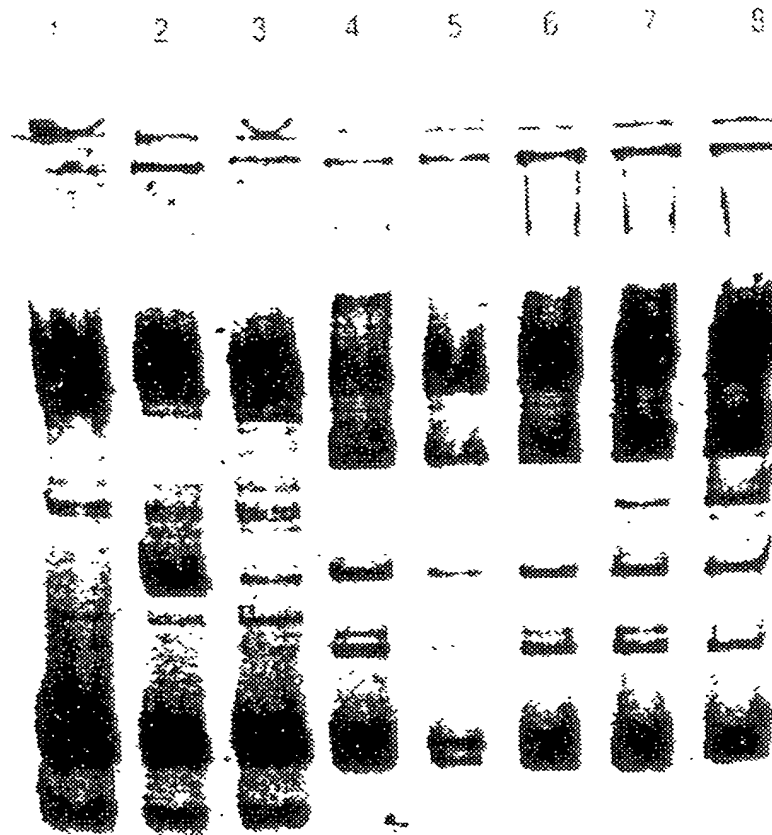


FIG. 93

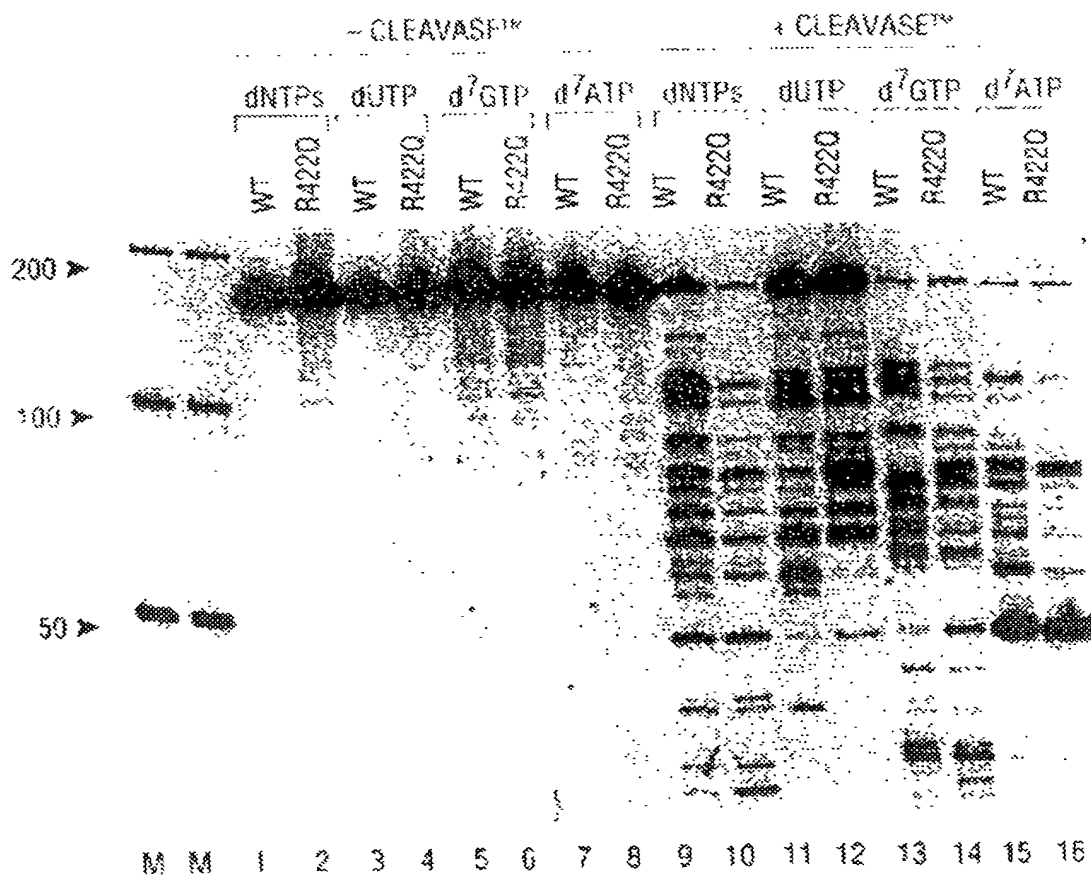


FIG. 94